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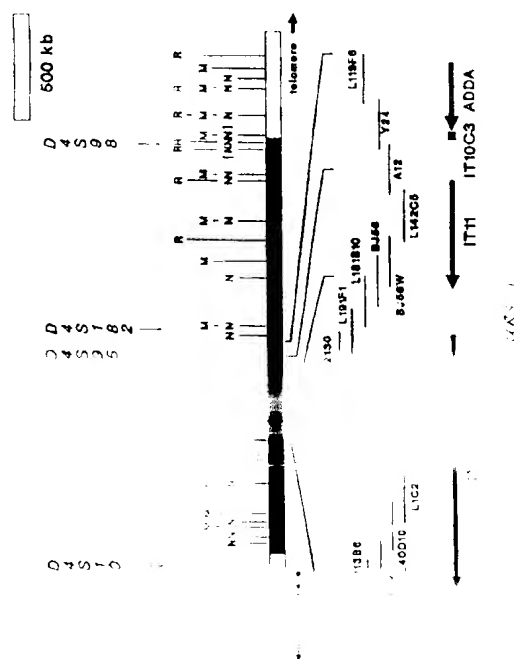
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(54) **Huntingtin DNA, protein and uses thereof.**

(57) A novel gene, *huntingtin*, is described, encoding huntingtin protein, recombinant vectors and hosts capable of expressing huntingtin. Methods for the diagnosis and treatment of Huntington's disease are also provided.



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Field of the Invention

The invention is in the field of the detection and treatment of genetic diseases. Specifically, the invention is directed to the *huntingtin* gene (also called the IT15 gene), huntingtin protein encoded by such gene, and the use of this gene and protein in assays (1) for the detection of a predisposition to develop Huntington's disease, (2) for the diagnosis of Huntington's disease (3) for the treatment of Huntington's disease, and (4) for monitoring the course of treatment of such treatment.

Background of the Invention

Huntington's disease (HD) is a progressive neurodegenerative disorder characterized by motor disturbance, cognitive loss and psychiatric manifestations (Martin and Gusella, *N. Engl. J. Med.* 315:1267-1276 (1986)). It is inherited in an autosomal dominant fashion, and affects about 1/10,000 individuals in most populations of European origin (Harper, P.S. *et al.*, in *Huntington's disease*, W.B. Saunders, Philadelphia, 1991). The hallmark of HD is a distinctive choreic movement disorder that typically has a subtle, insidious onset in the fourth to fifth decade of life and gradually worsens over a course of 10 to 20 years until death. Occasionally, HD is expressed in juveniles typically manifesting with more severe symptoms including rigidity and a more rapid course. Juvenile onset of HD is associated with a preponderance of paternal transmission of the disease allele. The neuropathology of HD also displays a distinctive pattern, with selective loss of neurons that is most severe in the caudate and putamen regions of the brain. The biochemical basis for neuronal death in HD has not yet been explained, and there is consequently no treatment effective in delaying or preventing the onset and progression of this devastating disorder.

The genetic defect causing HD was assigned to chromosome 4 in 1983 in one of the first successes of linkage analysis using polymorphic DNA markers in man (Gusella *et al.*, *Nature* 306:234-238 (1983)). Since that time, we have pursued a location cloning approach to isolating and characterizing the HD gene based on progressively refining its localization (Gusella, *FASEB J.* 3:2036-2041 (1989); Gusella, *Adv. Hum. Genet.* 20:125-151 (1991)). Among other work, this has involved the generation of new genetic markers in the region by a number of techniques (Pohl *et al.*, *Nucleic Acids Res.* 16:9185-9198 (1988); Whaley *et al.*, *Somat. Cell. Mol. Genet.* 17:83-91 (1991); MacDonald *et al.*, *J. Clin. Inv.* 84:1013-1016 (1989)), the establishment of genetic (MacDonald *et al.*, *Neuron* 3:183-190 (1989); Allitto *et al.*, *Genomics* 9:104-112 (1991)) and physical maps of the implicated regions (Bucan *et al.*, *Genomics* 6:1-15 (1990); Bates *et al.*, *Nature Genet.* 1:180-187 (1992); Doucette-Stamm *et al.*, *Somat. Cell Mol. Genet.* 17:471-480 (1991); Altherr *et al.*, *Genomics* 13:1040-1046 (1992)), the cloning of the 4p telomere of an HD chromosome in a YAC clone (Bates *et al.*, *Am. J. Hum. Genet.* 46:762-775 (1990); Youngman *et al.*, *Genomics* 14:350-356 (1992)), the establishment of YAC [yeast artificial chromosome] (Bates *et al.*, *Nature Genet.* 1:180-187 (1992)) and cosmid (Baxendale *et al.*, in preparation) contigs (a series of overlapping clones which together form a whole sequence) of the candidate region, as well as the analysis and characterization of a number of candidate genes from the region (Thompson *et al.*, *Genomics* 11:1133-1142 (1991); Taylor *et al.*, *Nature Genet.* 2:223-227 (1992); Ambrose *et al.*, *Hum. Mol. Genet.* 1:697-703 (1992)). Analysis of recombination events in HD kindreds has identified a candidate region of 2.2 Mb, between D4S10 and D4S98 in 4p16.3, as the most likely position of the HD gene (MacDonald *et al.*, *Neuron* 3:183-190 (1989); Bates *et al.*, *Am. J. Hum. Genet.* 49:7-16 (1991); Snell *et al.*, *Am. J. Hum. Genet.* 51:357-362 (1992)). Investigations of linkage disequilibrium between HD and DNA markers in 4p16.3 (Snell *et al.*, *J. Med. Genet.* 26:673-675 (1989); Theilman *et al.*, *J. Med. Genet.* 26:676-681 (1989)) have suggested that multiple mutations have occurred to cause the disorder (MacDonald *et al.*, *Am. J. Hum. Genet.* 49:723-734 (1991)). However, haplotype analysis using multi-allele markers has indicated that at least 1/3 of HD chromosomes are ancestrally related (MacDonald *et al.*, *Nature Genet.* 1: 99-103 (1992)). The haplotype shared by these HD chromosomes points to a 500 kb segment between D4S180 and D4S182 as the most likely site of the genetic defect.

Efforts to identify the HD gene have resulted in the identification of several candidate genes in the region. These include a novel G protein-coupled receptor kinase gene (IT11) in the central portion (Ambrose *et al.*, *Hum. Mol. Genet.* 1:697-703 (1992)). However, no defects implicating any of these genes as the HD locus have been found.

Summary of the Invention

A large gene, termed herein "huntingtin" or "IT15," has been identified that spans about 210 kb and encodes a previously undescribed protein of about 348 kDa. The huntingtin reading frame contains a polymorphic (CAG)_n trinucleotide repeat with at least 17 alleles in the normal population, varying from 11 to about 34 CAG copies. On HD chromosomes, the length of the trinucleotide repeat is substantially increased, for example, about 37 to at least 73 copies, and shows an apparent correlation with age of onset, the longest segments are detected in juvenile HD cases. The instability in length of the repeat is reminiscent of similar trinucleotide repeats in the fragile X syndrome and in myotonic dystrophy (Suthers *et al.*, *J. Med. Genet.* 29:761-765 (1992)).

The presence of an unstable, expandable trinucleotide repeat on HD chromosomes in the region of strongest linkage disequilibrium with the disorder suggests that this alteration underlies the dominant phenotype of HD, and that huntingtin encodes the HD gene.

The invention is directed to the protein huntingtin, DNA and RNA encoding this protein, and uses thereof. Accordingly, in a first embodiment, the invention is directed to purified preparations of the protein huntingtin, preferably substantially cell-free.

In a further embodiment, the invention is directed to a recombinant construct containing DNA or RNA encoding huntingtin.

In a further embodiment, the invention is directed to a vector containing such huntingtin-encoding nucleic acid.

In a further embodiment, the invention is directed to a host transformed with such vector.

In a further embodiment, the invention is directed to a method for producing huntingtin from such recombinant host.

In a further embodiment, the invention is directed to a method for diagnosing Huntington's disease using such huntingtin DNA, RNA and/or protein.

In a further embodiment, the invention is directed to a method for treating Huntington's disease using such huntingtin DNA, RNA and/or protein.

In a further embodiment, the invention is directed to a method of gene therapy of a symptomatic or pre-symptomatic patient, such method comprising providing a functional *huntingtin* gene with a (CAG)_n repeat of the normal range of 11-34 copies to the desired cells of such patient in need of such treatment, in a manner that permits the expression of the huntingtin protein provided by such gene, for a time and in a quantity sufficient to provide the huntingtin function to the cells of such patient.

In a further embodiment, the invention is directed to a method of gene therapy of a symptomatic or pre-symptomatic patient, such method comprising providing a functional *huntingtin* antisense gene to the desired cells of such patient in need of such treatment, in a manner that permits the expression of huntingtin antisense RNA provided by such gene, for a time and in a quantity sufficient to inhibit huntingtin mRNA expression in the cells of such patient.

In a further embodiment, the invention is directed to a method of gene therapy of a symptomatic or pre-symptomatic patient, such method comprising providing a functional *huntingtin* gene to the cells of such patient in need of such gene; in one embodiment the functional huntingtin gene contains a (CAG)_n repeat size between 11-34 copies.

In a further embodiment, the invention is directed to a method for diagnosing Huntington's disease or a predisposition to develop Huntington's disease in a patient, such method comprising determining the number of (CAG)_n repeats present in the huntingtin gene in such patient and especially in the affected tissue of such patient.

In a further embodiment, the invention is directed to a method for treating Huntington's disease in a patient, such method comprising decreasing the number of huntingtin (CAG)_n repeats in the huntingtin gene in the desired cells of such patient.

This is shown adapted from MacDonald *et al.*, 1992, *Nature Genet.* 1:483-488. The HD candidate region determined by recombination events is depicted as a hatched line between D4S10 and D4S98. The portion of the HD candidate region implicated as the site of the defect by linkage disequilibrium haplotype analysis (MacDonald *et al.*, *Nature Genet.* 1:99-103 (1992)) is shown as a filled box. Below the map schematic, the region from D4S180 to D4S182 is expanded to show the normal range of CAG repeat sizes (11-34) and the expanded range (37-73) found in HD patients.

The normal range of CAG repeat sizes is shown as a hatched line, and the expanded range (37-73) found in HD patients is shown as a filled box. The normal range of CAG repeat sizes is shown as a hatched line, and the expanded range (37-73) found in HD patients is shown as a filled box.

been used in HD families. The positions of *D4S127* and *D4S95* which form the core of haplotype in the region of maximum disequilibrium are also shown in the cosmid contig. Restriction sites are given for Not I (N), Mlu I (M) and Nru I (R). Sites displaying complete digestion are shown in boldface while sites subject to frequent incomplete digestion are shown as lighter symbols. Brackets around the "N" symbols indicate the presence of additional clustered Not I sites.

FIGURE 2. Northern blot analysis of the huntingtin (IT15) transcript. Results of the hybridization of IT15A to a Northern blot of RNA from normal (lane 1) and HD homozygous (lane 2 and 3) lymphoblasts are shown. A single RNA of about 11 kb was detected in all three samples, with slight apparent variations being due to unequal RNA concentrations. The HD homozygotes are independent, deriving from the large an American family (lane 2) and the large Venezuelan family (lane 3), respectively. The Venezuelan HD chromosome has a 4p16.3 haplotype of "5 2 2" defined by a (GT)_n polymorphism at *D4S127* and VNTR and TaqI RFLPs at *D4S95*. The American homozygote carries the most common 4p16.3 haplotype found on HD chromosomes: "2 11 1" (MacDonald *et al.*, *Nature Genet.* 1:99-103 (1992)).

FIGURE 3. Schematic of cDNA clones defining the IT15 transcript. Five cDNAs are represented under a schematic of the composite IT15 sequence. The thin line corresponds to untranslated regions. The thick line corresponds to coding sequence, assuming initiation of translation at the first Met codon in the open reading frame. Stars mark the positions of the following exon clones 5' to 3': DL83D3-8, DL83D3-1, DL228B6-3, DL228B6-5, DL228B6-13, DL69F7-3, DL178H4-6, DL118F5-U and DL134B9-U4.

The composite sequence was derived as follows. From 22 bases 3' to the putative initiator Met ATG, the sequence was compiled from the cDNA clones and exons shown. There are 9 bases of sequence intervening between the 3' end of IT16B and the 5' end of IT15B. These were by PCR amplification of first strand cDNA and sequencing of the PCR product. At the 5' end of the composite sequence, the cDNA clone IT16C terminates 27 bases upstream of the (CAG)_n. However, when IT16C was identified, we had already generated genomic sequence surrounding the (CAG)_n in an attempt to generate new polymorphisms. This sequence matched the IT16C sequence, and extended it 337 bases upstream, including the apparent Met initiation codon.

FIGURE 4. Composite sequence of huntingtin (IT15)(SEQ ID NO:5 and SEQ ID NO:6). The composite DNA sequence of huntingtin (IT15) is shown (SEQ ID NO:5). The predicted protein product (SEQ ID NO:6) is shown below the DNA sequence, based on the assumption that translation begins at the first in-frame methionine of the long open reading frame.

FIGURE 5. DNA sequence analysis of the (CAG)_n repeat. DNA sequence shown in panels 1, 2 and 3, demonstrates the variation in the (CAG)_n repeat detected in normal cosmid L191F1 (1), cDNA IT16C (2), and HD cosmid GUS72-2130. Panels 1 and 3 were generated by direct sequencing of cosmid subclones using the following primer (SEQ ID NO:1):

5' GGC GGG AGA CCG CCA TGG CG 3'.

Panel 2 was generated using the pBSKII T7 primer (SEQ ID NO:2):

5' AAT ACG ACT CAC TAT AG 3'.

FIGURE 6. PCR analysis of the (CAG)_n repeat in a Venezuelan HD sibship with some offspring displaying juvenile onset. Results of PCR analysis of a sibship in the Venezuela HD pedigree are shown. Affected individuals are represented by shaded symbols. Progeny are shown as triangles for confidentiality. AN1, AN2 and AN3 mark the positions of the allelic products from normal chromosomes. AE marks the range of PCR products from the HD chromosome. The intensity of background constant bands, which represent a useful reference for comparison of the above PCR products, varies with slight differences in PCR conditions. The PCR products from cosmids L191F1 and GUS72-2130 are loaded in lanes 12 and 13 and have 18 and 48 CAG repeats, respectively.

Information is given to preserve the blind status of investigators in the Venezuelan Collaborative Group. AN1 and AN2 mark the positions of the allelic products from normal parental chromosomes. AE marks the range of PCR products from the HD chromosome. The PCR products from cosmids L191F1 and GUS72-2130 are loaded in lanes 29 and 30 and have 18 and 48 CAG repeats, respectively.

FIGURE 8. PCR analysis of the (CAG)_n repeat in a Venezuelan HD sibship with some offspring displaying juvenile onset. Results of PCR analysis of a sibship in the Venezuela HD pedigree are shown. Affected individuals are represented by shaded symbols. Progeny are shown as triangles for confidentiality. AN1, AN2 and AN3 mark the positions of the allelic products from normal chromosomes. AE marks the range of PCR products from the HD chromosome. The PCR products from cosmids L191F1 and GUS72-2130 are loaded in lanes 29 and 30 and have 18 and 48 CAG repeats, respectively.

4, 5, 7 and 8 represent PCR products from related HD heterozygotes. Lane 2 contains the PCR products from a member of the family homozygous for the same HD chromosome. Lane 6 contains PCR products from a normal individual. Pedigree relationships and affected status are not presented to preserve confidentiality. The PCR products from cosmids L191F1 and GUS72-2130 (which was derived from the individual represented in lane 2) are loaded in lanes 9 and 10 and have 18 and 48 CAG repeats, respectively.

FIGURES 9 and 10. PCR analysis of the (CAG)_n repeat in two families with supposed new mutation causing HD. Results of PCR analysis of two families in which sporadic HD cases representing putative new mutants are shown. Individuals in each pedigree are numbered by generation (Roman numerals) and order in the pedigree. Triangles are used to protect confidentiality. Filled symbols indicate symptomatic individuals. The different chromosomes segregating in the pedigree have been distinguished by extensive typing with polymorphic markers in 4p16.3 and have been assigned arbitrary numbers shown above the gel lanes. The starred chromosomes (3 in Figure 9, 1 in Figure 10) represent the presumed HD chromosome. AN denotes the range of normal alleles; AE denotes the range of alleles present in affected individuals and in their unaffected relatives bearing the same chromosomes.

FIGURE 11. Comparison of (CAG)_n Repeat Unit Number on Control and HD Chromosomes. Frequency distributions are shown for the number of (CAG)_n repeat units observed on 425 HD chromosomes from 150 independent families, and from 545 control chromosomes.

FIGURE 12. Comparison of (CAG)_n Repeat Unit Number on Maternally and Paternally Transmitted HD Chromosomes. Frequency distributions are shown for the 134 and 161 HD chromosomes from Figure 11 known to have been transmitted from the mother (Panel A) and father (Panel B), respectively. The two distributions differ significantly based on a t-test ($t_{272.3} = 5.34$, $p < 0.0001$).

FIGURE 13. Comparison of (CAG)_n Repeat Unit Number on HD Chromosomes from Three Large Families with Different HD Founders. Frequency distributions are shown for 75, 25 and 35 HD chromosomes from the Venezuelan HD family (Panel A) (Gusella, J.F., *et al.*, *Nature* 306:234-238 (1983); Wexler, N.S., *et al.*, *Nature* 326:194-197 (1987)), Family Z (Panel B) and Family D (Panel C) (Folstein, S.E., *et al.*, *Science* 229:776-779 (1985)), respectively. The Venezuelan distribution did not differ from the overall HD chromosome distribution in Figure 11 ($t_{79.7} = 1.58$, $p < 0.12$). Both Family Z and Family D did produce distributions significantly different from the overall HD distribution ($t_{42.2} = 6.73$, $p < 0.0001$ and $t_{48.8} = 2.90$, $p < 0.004$, respectively).

Figure 14. Relationship of (CAG)_n Repeat Length in Parents and Corresponding Progeny. Repeat length on the HD chromosome in mothers (Panel A) or fathers (Panel B) is plotted against the repeat length in the corresponding offspring. A total of 25 maternal transmissions and 37 paternal transmissions were available for typing.

FIGURE 15. Amplification of the HD (CAG)_n Repeat From Sperm and Lymphoblast DNA. DNA from sperm (S) and lymphoblasts (L) for 5 members (pairs 1-5) of the Venezuelan HD pedigree aged 24-30 were used for PCR amplification of the HD (CAG)_n repeat. The lower band in each lane derives from the normal chromosome.

FIGURE 16. Relationship of Repeat Unit Length with Age of Onset. Age of onset was established for 234 diagnosed HD gene carriers and plotted against the repeat length observed on both the HD and normal chromosomes in the corresponding lymphoblast lines.

Detailed Description of the Invention

In the following description, reference will be made to various methodologies known to those of skill in the art of molecular genetics and biology. Publications and other materials setting forth such known methodologies to which reference is made are incorporated herein by reference in their entireties as though set forth in full.

The IT15 gene described herein is a gene from the proximal portion of the 500 kb segment between human chromosome 4 markers *D4S180* and *D4S182*. The huntingtin gene spans about 210 kb of DNA and encodes a previously undescribed protein of about 348 kDa. The huntingtin reading frame contains a polymorphic (CAG)_n trinucleotide repeat with at least 17 alleles in the human population.

These results indicate that the number of CAG repeats in the huntingtin gene increases to a range of 37 to at least 86 copies. These results are the basis of a conclusion that the huntingtin gene encodes a protein called "huntingtin," and that in such huntingtin gene the increase in the number of CAG repeats to a range of greater than about 37 repeats is the alteration that underlies the dominant phenotype of Huntington's disease.

As used herein huntingtin gene is also called the Huntington's disease gene.

The invention is directed to the identification of the huntingtin gene, and to the identification of the huntingtin gene in a family with a history of Huntington's disease, and to the identification of the huntingtin gene in a family with a history of Huntington's disease, and to the identification of the huntingtin gene in a family with a history of Huntington's disease, and to the identification of the huntingtin gene in a family with a history of Huntington's disease.

1. Cloning Of Huntingtin DNA And Expression Of Huntingtin Protein

The identification of huntingtin DNA and protein as the altered gene in Huntington's disease patients is exemplified below. In addition to utilizing the exemplified methods and results for the identification of deletions of the *huntingtin* gene in Huntington's disease patients, and for the isolation of the native human *huntingtin* gene, the sequence information presented in Figure 4 represents a nucleic acid and protein sequence, that, when inserted into a linear or circular recombinant nucleic acid construct such as a vector, and used to transform a host cell, will provide copies of *huntingtin* DNA and huntingtin protein that are useful sources for the native *huntingtin* DNA and huntingtin protein for the methods of the invention. Such methods are known in the art and are briefly outlined below.

The process for genetically engineering the *huntingtin* coding sequence, for expression under a desired promoter, is facilitated through the cloning of genetic sequences which are capable of encoding such huntingtin protein. Such cloning technologies can utilize techniques known in the art for construction of a DNA sequence encoding the huntingtin protein, such as, for example, polymerase chain reaction technologies utilizing the *huntingtin* sequence disclosed herein to isolate the *huntingtin* gene anew, or an allele thereof that varies in the number of CAG repeats in such gene, or polynucleotide synthesis methods for constructing the nucleotide sequence using chemical methods. Expression of the cloned *huntingtin* DNA provides huntingtin protein.

As used herein, the term "genetic sequences" is intended to refer to a nucleic acid molecule of DNA or RNA, preferably DNA. Genetic sequences that are capable of being operably linked to DNA encoding huntingtin protein, so as to provide for its expression and maintenance in a host cell are obtained from a variety of sources, including commercial sources, genomic DNA, cDNA, synthetic DNA, and combinations thereof. Since the genetic code is universal, it is to be expected that any DNA encoding the huntingtin amino acid sequence of the invention will be useful to express huntingtin protein in any host, including prokaryotic (bacterial) hosts, eukaryotic hosts (plants, mammals (especially human), insects, yeast, and especially any cultured cell populations).

If it is desired to select anew a gene encoding huntingtin from a library that is thought to contain a *huntingtin* gene, such library can be screened and the desired gene sequence identified by any means which specifically selects for a sequence coding for the *huntingtin* gene or expressed huntingtin protein such as, for example, a) by hybridization (under stringent conditions for DNA:DNA hybridization) with an appropriate *huntingtin* DNA probe(s) containing a sequence specific for the DNA of this protein, such sequence being that provided in Figure 4 or a functional derivative thereof that is, a shortened form that is of sufficient length to identify a clone containing the *huntingtin* gene, or b) by hybridization-selected translational analysis in which native *huntingtin* mRNA which hybridizes to the clone in question is translated *in vitro* and the translation products are further characterized for the presence of a biological activity of huntingtin, or c) by immunoprecipitation of a translated huntingtin protein product from the host expressing the huntingtin protein.

When a human allele does not encode the identical sequence to that of Figure 4, it can be isolated and identified as being *huntingtin* DNA using the same techniques used herein, and especially PCR techniques to amplify the appropriate gene with primers based on the sequences disclosed herein. Many polymorphic probes useful in the fine localization of genes on chromosome 4 are known and available (see, for example, 40 "ATCC/NIH Repository Catalogue of Human and Mouse DNA Probes and Libraries," fifth edition, 1991, pages 4-6. For example, a useful D4S10 probe is clone designation pTV20 (ATCC 57605 and 57604); H5.52 (ATCC 61107 and 61106) and F5.53 (ATCC 61108).

Human chromosome 4-specific libraries are known in the art and available from the ATCC for the isolation of probes ("ATCC/NIH Repository Catalogue of Human and Mouse DNA Probes and Libraries," fifth edition, 1991, pages 72-73), for example, LL04NS01 and LL04NS02 (ATCC 57719 and ATCC57718) are useful for these purposes.

It is not necessary to utilize the exact vector constructs exemplified in the invention; equivalent vectors can be constructed using techniques known in the art. For example, the vector pUC19 (see, e.g., Sambrook et al., 1989) can be used in place of the pUC18 vector.

huntingtin genomic DNA may or may not include naturally occurring introns. Moreover, such genomic DNA can be obtained in association with the native *huntingtin* 5' promoter region of the gene sequences and/or with the native *huntingtin* 3' transcriptional termination region.

Such *huntingtin* genomic DNA can also be obtained in association with the genetic sequences which are
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5' and/or 3' non-transcribed regions of the native *huntingtin* gene, and/or, the 5' and/or 3' non-translated regions of the huntingtin mRNA can be retained and employed for transcriptional and translational regulation.

Genomic DNA can be extracted and purified from any host cell, especially a human host cell possessing chromosome 4, by means well known in the art. Genomic DNA can be shortened by means known in the art, such as physical shearing or restriction digestion, to isolate the desired *huntingtin* gene from a chromosomal region that otherwise would contain more information than necessary for the utilization of the *huntingtin* gene in the hosts of the invention. For example, restriction digestion can be utilized to cleave the full-length sequence at a desired location. Alternatively, or in addition, nucleases that cleave from the 3'-end of a DNA molecule can be used to digest a certain sequence to a shortened form, the desired length then being identified and purified by polymerase chain reaction technologies, gel electrophoresis, and DNA sequencing. Such nucleases include, for example, Exonuclease III and *Bal31*. Other nucleases are well known in the art.

Alternatively, if it is known that a certain host cell population expresses huntingtin protein, then cDNA techniques known in the art can be utilized to synthesize a cDNA copy of the huntingtin mRNA present in such population.

For cloning the genomic or cDNA nucleic acid that encodes the amino acid sequence of the huntingtin protein into a vector, the DNA preparation can be ligated into an appropriate vector. The DNA sequence encoding huntingtin protein can be inserted into a DNA vector in accordance with conventional techniques, including blunt-ending or staggered-ending termini for ligation, restriction enzyme digestion to provide appropriate termini, filling in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and ligation with appropriate ligases. Techniques for such manipulations are well known in the art.

When the huntingtin DNA coding sequence and an operably linked promoter are introduced into a recipient eukaryotic cell (preferably a human host cell) as a non-replicating, non-integrating, molecule, the expression of the encoded huntingtin protein can occur through the transient (nonstable) expression of the introduced sequence.

Preferably the coding sequence is introduced on a DNA molecule, such as a closed circular or linear molecule that is capable of autonomous replication. If integration into the host chromosome is desired, it is preferable to use a linear molecule. If stable maintenance of the *huntingtin* gene is desired on an extrachromosomal element, then it is preferable to use a circular plasmid form, with the appropriate plasmid element for autonomous replication in the desired host.

The desired gene construct, providing a gene coding for the huntingtin protein, and the necessary regulatory elements operably linked thereto, can be introduced into a desired host cells by transformation, transfection, or any method capable of providing the construct to the host cell. A marker gene for the detection of a host cell that has accepted the *huntingtin* DNA can be on the same vector as the *huntingtin* DNA or on a separate construct for cotransformation with the huntingtin coding sequence construct into the host cell. The nature of the vector will depend on the host organism.

Suitable selection markers will depend upon the host cell. For example, the marker can provide biocide resistance, e.g., resistance to antibiotics, or heavy metals, such as copper, or the like.

Factors of importance in selecting a particular plasmid or viral vector include: the ease with which recipient cells that contain the vector can be recognized and selected from those recipient cells which do not contain the vector; the number of copies of the vector which are desired in a particular host; and whether it is desirable to be able to "shuttle" the vector between host cells of different species.

When it is desired to use *S. cerevisiae* as a host for a shuttle vector, preferred *S. cerevisiae* yeast plasmids include those containing the 2-micron circle, etc., or their derivatives. Such plasmids are well known in the art and are commercially available.

Oligonucleotide probes specific for the *huntingtin* sequence can be used to identify clones to huntingtin and can be designed *de novo* from the knowledge of the amino acid sequence of the protein as provided herein in Figure 4 or from the knowledge of the nucleic acid sequence of the DNA encoding such protein as provided herein in Figure 4 or of a related protein. Alternatively, the

present invention provides a vector construct which expresses a huntingtin protein of the amino acid sequence set forth in Table I. The vector construct contains expression control sequences which contain transcriptional regulatory information and such sequences are "operably linked" to the huntingtin nucleotide sequence which encode the huntingtin polypeptide.

An operable linkage is a linkage in which a sequence is connected to a regulatory sequence by a linker sequence which is capable of being transcribed and translated. The linker sequence is a DNA sequence which is capable of being transcribed and translated and is operably linked to the 5' end of the coding sequence. The linker sequence is operably linked if induction of promoter function results in the transcription of mRNA

encoding the desired protein and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the expression regulatory sequences to direct the expression of the protein, antisense RNA, or (3) interfere with the ability of the DNA template to be transcribed. Thus, a promoter region would be operably linked to a DNA sequence if the promoter

5 was capable of effecting transcription of that DNA sequence.

The precise nature of the regulatory regions needed for gene expression can vary between species or cell types, but shall in general include, as necessary, 5' non-transcribing and 5' non-translating (non-coding) sequences involved with initiation of transcription and translation respectively, such as the TATA box, capping sequence, CAAT sequence, and the like, with those elements necessary for the promoter sequence being provided by the promoters of the invention. Such transcriptional control sequences can also include enhancer sequences or upstream activator sequences, as desired.

The vectors of the invention can further comprise other operably linked regulatory elements such as DNA elements which confer antibiotic resistance, or origins of replication for maintenance of the vector in one or more host cells.

15 In another embodiment, especially for maintenance of the vectors of the invention in prokaryotic cells, or in yeast *S. cerevisiae* cells, the introduced sequence is incorporated into a plasmid or viral vector capable of autonomous replication in the recipient host. Any of a wide variety of vectors can be employed for this purpose. In *Bacillus* hosts, integration of the desired DNA can be necessary.

Expression of a protein in eukaryotic hosts such as a human cell requires the use of regulatory regions functional in such hosts. A wide variety of transcriptional and translational regulatory sequences can be employed, depending upon the nature of the host. Preferably, these regulatory signals are associated in their native state with a particular gene which is capable of a high level of expression in the specific host cell, such as a specific human tissue type. In eukaryotes, where transcription is not linked to translation, such control regions may or may not provide an initiator methionine (AUG) codon, depending on whether the cloned sequence contains such a methionine. Such regions will, in general, include a promoter region sufficient to direct the initiation of RNA synthesis in the host cell.

If desired, the non-transcribed and/or non-translated regions 3' to the sequence coding for the huntingtin protein can be obtained by the above-described cloning methods. The 3'-non-transcribed region of the native human *huntingtin* gene can be retained for its transcriptional termination regulatory sequence elements, or for those elements which direct polyadenylation in eukaryotic cells. Where the native expression control sequences signals do not function satisfactorily in a host cell, then sequences functional in the host cell can be substituted.

It may be desired to construct a fusion product that contains a partial coding sequence (usually at the amino terminal end) of a first protein or small peptide and a second coding sequence (partial or complete) of the huntingtin protein at the carboxyl end. The coding sequence of the first protein can, for example, function as a signal sequence for secretion of the huntingtin protein from the host cell. Such first protein can also provide for tissue targeting or localization of the huntingtin protein if it is to be made in one cell type in a multicellular organism and delivered to another cell type in the same organism. Such fusion protein sequences can be designed with or without specific protease sites such that a desired peptide sequence is amenable to subsequent removal.

The expressed huntingtin protein can be isolated and purified from the medium of the host in accordance with conventional conditions, such as extraction, precipitation, chromatography, affinity chromatography, electrophoresis, or the like. For example, affinity purification with anti-huntingtin antibody can be used. A protein having the amino acid sequence shown in Figure 3 can be made, or a shortened peptide of this sequence can be made, and used to raised antibodies using methods well known in the art. These antibodies can be used to affinity purify or quantitate huntingtin protein from any desired source.

If it is necessary to extract huntingtin protein from the intracellular regions of the host cells, the host cells can be collected by centrifugation, or with suitable buffers, lysed, and the intracellular contents extracted.

Use Of Huntingtin For Diagnostic And Treatment Purposes

55 It is to be understood that although the following discussion is specifically directed to human patients, the teachings are also applicable to any animal that expresses huntingtin and in which alteration of huntingtin or, especially, the up-regulation of CAG repeats, is associated with the development of a neurodegenerative disease.

2. *Diagnosis of Huntington's Disease*

Huntington's disease (HD) is a neurodegenerative

It is also to be understood that the methods referred to herein are applicable to any patient suspected of developing/having Huntington's disease, whether such condition is manifest at a young age or at a more advanced age in the patient's life. It is also to be understood that the term "patient" does not imply that symptoms are present, and patient includes any individual it is desired to examine or treat using the methods of the invention.

The diagnostic and screening methods of the invention are especially useful for a patient suspected of being at risk for developing Huntington's disease based on family history, or a patient in which it is desired to diagnose or eliminate the presence of the Huntington's disease condition as a causative agent behind a patient's symptoms.

It is to be understood that to the extent that a patient's symptoms arise due to the alteration of the CAG repeat copy numbers in the *huntingtin* gene, even without a diagnosis of Huntington's disease, the methods of the invention can identify the same as the underlying basis for such condition.

According to the invention, presymptomatic screening of an individual in need of such screening for their likelihood of developing Huntington's disease is now possible using DNA encoding the huntingtin gene of the invention, and specifically, DNA having the sequence of the normal human huntingtin gene. The screening method of the invention allows a presymptomatic diagnosis, including prenatal diagnosis, of the presence of an aberrant *huntingtin* gene in such individuals, and thus an opinion concerning the likelihood that such individual would develop or has developed Huntington's disease or symptoms thereof. This is especially valuable for the identification of carriers of altered huntingtin gene alleles where such alleles possess an increased number of CAG repeats in their huntingtin gene, for example, from individuals with a family history of Huntington's disease. Especially useful for the determination of the number of CAG repeats in the patient's *huntingtin* gene is the use of PCR to amplify such region or DNA blotting techniques.

For example, in the method of screening, a tissue sample would be taken from such individual, and screened for (1) the presence of the 'normal' human *huntingtin* gene, especially for the presence of a "normal" range of 11-34 CAG copies in such gene. The human *huntingtin* gene can be characterized based upon, for example, detection of restriction digestion patterns in 'normal' versus the patient's DNA, including RFLP analysis, using DNA probes prepared against the *huntingtin* sequence (or a functional fragment thereof) taught in the invention. Similarly, huntingtin mRNA can be characterized and compared to normal huntingtin mRNA (a) levels and/or (b) size as found in a human population not at risk of developing Huntington's disease using similar probes. Lastly, huntingtin protein can be (a) detected and/or (b) quantitated using a biological assay for huntingtin, for example, using an immunological assay and anti-huntingtin antibodies. When assaying huntingtin protein, the immunological assay is preferred for its speed. Methods of making antibody against the huntingtin are well known in the art.

An (1) aberrant *huntingtin* DNA size pattern, such as an aberrant *huntingtin* RFLP, and/or (2) aberrant huntingtin mRNA sizes or levels and/or (3) aberrant huntingtin protein levels would indicate that the patient has developed or is at risk for developing a huntingtin-associated symptom such as a symptom associated with Huntington's disease.

The screening and diagnostic methods of the invention do not require that the entire huntingtin DNA coding sequence be used for the probe. Rather, it is only necessary to use a fragment or length of nucleic acid that is sufficient to detect the presence of the huntingtin gene in a DNA preparation from a normal or affected individual, the absence of such gene, or an altered physical property of such gene (such as a change in electrophoretic migration pattern).

Prenatal diagnosis can be performed when desired, using any known method to obtain fetal cells, including amniocentesis, chorionic villous sampling (CVS), and fetoscopy. Prenatal chromosome analysis can be used to determine if the portion of chromosome 4 possessing the normal *huntingtin* gene is present in a heterozygous state, and PCR amplification or DNA blotting utilized for estimating the size of the CAG repeat in the *huntingtin* gene.

The huntingtin DNA can be synthesized, especially, the CAG repeat region can be amplified by PCR.

In one method of treating Huntington's disease in a patient in need of such treatment, functional *huntingtin* DNA is provided to the cells of such patient, preferably prior to such symptomatic state that indicates the death of many of the patient's neuronal cells which it is desired to target with the method of the invention. The replacement *huntingtin* DNA is provided in a vector and an agent that causes the expression of the huntingtin gene. The provided DNA is taken up by the cells in a quantity sufficient to cause the expression of the huntingtin gene. The provided DNA is delivered to target patients in need of a gene or protein missing from the

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Although the method is specifically described for DNA-DNA probes, it is to be understood that RNA possessing the same sequence information as the DNA of the invention can be used when desired.

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Of special interest to the present invention are antibodies to huntingtin (or their functional derivatives) which are produced in humans, or are "humanized" (i.e. non-immunogenic in a human) by recombinant or other technology. Humanized antibodies may be produced from hybridomas or by recombinant DNA technology.

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(Jones, P.T. *et al.*, *Nature* 321:552-525 (1986); Verhoeyan *et al.*, *Science* 239:1534 (1988); Beidler, C.B. *et al.*, *J. Immunol.* 141:4053-4060 (1988)).

In another embodiment, the present invention relates to a hybridoma which produces the above-described monoclonal antibody, or binding fragment thereof. A hybridoma is an immortalized cell line which is capable of secreting a specific monoclonal antibody.

In general, techniques for preparing monoclonal antibodies and hybridomas are well known in the art (Campbell, *"Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology,"* Elsevier Science Publishers, Amsterdam, The Netherlands (1984); St. Groth *et al.*, *J. Immunol. Methods* 35:1-21 (1980)).

Any animal (mouse, rabbit, and the like) which is known to produce antibodies can be immunized with the selected polypeptide. Methods for immunization are well known in the art. Such methods include subcutaneous or interperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of polypeptide used for immunization will vary based on the animal which is immunized, the antigenicity of the polypeptide and the site of injection.

The polypeptide may be modified or administered in an adjuvant in order to increase the peptide antigenicity. Methods of increasing the antigenicity of a polypeptide are well known in the art. Such procedures include coupling the antigen with a heterologous protein (such as globulin or β -galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells.

Any one of a number of methods well known in the art can be used to identify the hybridoma cell which produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, western blot analysis, or radioimmunoassay (Lutz *et al.*, *Exp. Cell Res.* 175:109-124 (1988)).

Hybridomas secreting the desired antibodies are cloned and the class and subclass is determined using procedures known in the art (Campbell, *Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology, supra* (1984)).

For polyclonal antibodies, antibody containing antisera is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures.

In another embodiment of the present invention, the above-described antibodies are detectably labeled. Antibodies can be detectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, and the like), enzymatic labels (such as horse radish peroxidase, alkaline phosphatase, and the like) fluorescent labels (such as FITC or rhodamine, and the like), paramagnetic atoms, and the like. Procedures for accomplishing such labeling are well-known in the art, for example, see (Sternberger *et al.*, *J. Histochem. Cytochem.* 18:315 (1970); Bayer *et al.*, *Meth. Enzym.* 62:308 (1979); Engval *et al.*, *Immunol.* 109:129 (1972); Goding, *J. Immunol. Meth.* 13:215 (1976)). The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays to identify cells or tissues which express a specific peptide.

In another embodiment of the present invention the above-described antibodies are immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir *et al.*, *"Handbook of Experimental Immunology"* 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10 (1986); Jacoby *et al.*, *Meth. Enzym.* 34 Academic Press, N.Y. (1974)). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as in immunochromatography.

Furthermore, one skilled in the art can readily adapt currently available procedures, as well as the techniques, methods and kits disclosed above with regard to antibodies, to generate peptides capable of binding to a specific peptide sequence in order to generate rationally designed antipeptide peptides, for example see Hurby *et al.* "Application of Synthetic Peptides: Antisense Peptides", *Cell and Tissue Research*, 241:1-10 (1985).

According to the present invention, the amino acid sequence of the huntingtin peptide is modified to produce a modified peptide.

One embodiment of the present invention is a modified peptide wherein the basic amino acid residues found in the huntingtin peptide sequence with acidic residues, while maintaining hydrophobic and uncharged polar groups. For example, lysine, arginine, and/or histidine residues are replaced with aspartic acid or glutamic acid and glutamic acid residues are replaced by lysine, arginine or histidine.

The manner and method of carrying out the present invention can be more fully understood by reference to the following examples which are given by way of illustration and not by way of limitation. The examples are given for illustrative purposes only and are not intended to limit the scope of the present invention.

Examples

The gene causing Huntington's disease has been mapped in 4p16.3 but has previously eluded identification. The invention uses haplotype analysis of linkage disequilibrium to spotlight a small segment of 4p16.3 as the likely location of the defect. A new gene, *huntingtin* (*IT15*), isolated using cloned "trapped" exons from a cosmid contig of the target area contains a polymorphic trinucleotide repeat that is expanded and unstable on HD chromosomes. A (CAG)_n repeat longer than the normal range of about 11 to about 34 copies was observed on HD chromosomes from all 75 disease families examined, comprising a wide range of ethnic backgrounds and 4p16.3 haplotypes. The (CAG)_n repeat, which varies from 37 to at least 86 copies on HD chromosomes appears to be located within the coding sequence of a predicted about 348 kDa protein that is widely expressed but unrelated to any known gene. Thus, the Huntington's disease mutation involves an unstable DNA segment, similar to those described in fragile X syndrome and myotonic dystrophy, acting in the context of a novel 4p16.3 gene to produce a dominant phenotype.

The following protocols and experimental details are referenced in the examples that follow.

HD Cell Lines. Lymphoblast cell lines from HD families of varied ethnic backgrounds used for genetic linkage and disequilibrium studies (Conneally *et al.*, *Genomics* 5:304-308 (1989); MacDonald *et al.*, *Nature Genet.* 1:99-103 (1992)) have been established (Anderson and Gusella, *In Vitro* 20:856-858 (1984)) in the Molecular Neurogenetics Unit, Massachusetts General Hospital, over the past 13 years. The Venezuelan HD pedigree is an extended kindred of over 10,000 members in which all affected individuals have inherited the HD gene from a common founder (Gusella *et al.*, *Nature* 306:234-238 (1983); Gusella *et al.*, *Science* 225:1320-1326 (1984); Wexler *et al.*, *Nature* 326:194-197 (1987)).

DNA/RNA Blotting. DNA was prepared from cultured cells and DNA blots prepared and hybridized as described (Gusella *et al.*, *Proc. Natl. Acad. Sci. USA* 76:5239-5243 (1979); Gusella *et al.*, *Nature* 306:234-238 (1983)). RNA was prepared and Northern blotting performed as described in Taylor *et al.*, *Nature Genet.* 3:223-227 (1992).

Construction of Cosmid Contig. The initial construction of the cosmid contig was by chromosome walking from cosmids L19 and BJ56 (Allitto *et al.*, *Genomics* 9:104-112 (1991); Lin *et al.*, *Somat. Cell Mol. Genet.* 17:481-488 (1991)). Two libraries were employed, a collection of Alu-positive cosmids from the reduced cell hybrid H39-8C10 (Whaley *et al.*, *Som. Cell Mol. Genet.* 17:83-91 (1991)) and an arrayed flow-sorted chromosome 4 cosmid library (NM87545) provided by the Los Alamos National Laboratory. Walking was accomplished by hybridization of whole cosmid DNA, using suppression of repetitive and vector sequences, to robot-generated high density filter grids (Nizetic, D. *et al.*, *Proc. Natl. Acad. Sci. USA* 88:3233-3237 (1991); Lehrach, H. *et al.*, in *Genome Analysis: Genetic and Physical Mapping, Volume 1*, Davies, K.E. *et al.*, Ed., Cold Spring Harbor Laboratory Press, 1991, pp. 39-81). Cosmids L1C2, L69F7, L228B6 and L83D3 were first identified by hybridization of YAC clone YGA2 to the same arrayed library (Bates *et al.*, *Nature Genet.* 1:180-187 (1992); Baxendale *et al.*, *Nucleic Acids Res.* 19:6651 (1991)). HD cosmid GUS72-2130 was isolated by standard screening of a GUS72 cosmid library using a single-copy probe. Cosmid overlaps were confirmed by a combination of clone-to-clone and clone-to-genomic hybridizations, single-copy probe hybridizations and restriction mapping.

cDNA Isolation and Characterization. Exon probes were isolated and cloned as described (Buckler *et al.*, *Proc. Natl. Acad. Sci. USA* 88:4005-4009 (1991)). Exon probes and cDNAs were used to screen human lambdaZAPII cDNA libraries constructed from adult frontal cortex, fetal brain, adenovirus transformed retinal cell line RCA, and liver RNA. cDNA clones, PCR products and trapped exons were sequenced as described (Sanger *et al.*, *Proc. Natl. Acad. Sci. USA* 74:5463-5467 (1977)). Direct cosmid sequencing was performed as described (McClatchey *et al.*, *Hum. Mol. Genet.* 1:521-527 (1992)). Database searches were performed using the BLAST network service of National Center for Biotechnology Information (Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990)).

PCR Assay of the (CAG)_n Repeat. The (CAG)_n repeat was amplified by PCR using the following primers:

and

5' AAA CTC ACG GTC GGT GCA GCG GCT CCT CAG 3'

The PCR reaction mixture contained 100 ng of genomic DNA, 100 mM Tris-HCl, pH 8.8, 50 mM KCl, 2 mM MgCl₂, 0.1% Triton X-100, 0.01% Tween-20, 0.01% SDS, 0.01% NP-40, 0.01% BSA, 0.01% DMSO, 0.1 unit Perfectmatch (Stratagene) and 1.25 units of Taq polymerase.

tagene), 2.5 μ Ci 32 P-dCTP (Amersham) and 1.25 units Taq polymerase (Boehringer Mannheim). After heating to 94°C for 1.5 minutes, the reaction mix was cycled according to the following program: 40 X [1'@94°C; 1'@60°C; 2'@72°C]. 5 μ l of each PCR reaction was diluted with an equal volume of 95 % formamide loading dye and heat denatured for 2 min. at 95°C. The products were resolved on 5 % denaturing polyacrylamide gels. The PCR product from this reaction using cosmid L191F1 (CAG₁₈) as template was 247 bp. Allele sizes were estimated relative to a DNA sequencing ladder, the PCR products from sequenced cosmids, and the invariant background bands often present on the gel. Estimates of allelic variation were obtained by typing unrelated individuals of largely Western European ancestry, and normal parents of affected HD individuals from various pedigrees.

Typing of HD and normal chromosomes in Examples 5-8. HD chromosomes were derived from symptomatic individuals and "at risk" individuals known to be gene carriers by linkage marker analysis. All HD chromosomes were from members of well-characterized HD families of varied ethnic backgrounds used previously for genetic linkage and disequilibrium studies (MacDonald, M.E., *et al.*, *Nature Genet.* 1:99-103 (1992); Conneally, P.M., *et al.*, *Genomics* 5:304-308 (1989)). Three of the 150 families used were large pedigrees, each descended from a single founder. The large Venezuelan HD pedigree is an extended kindred of over 13,000 members from which we typed 75 HD chromosomes (Gusella, J.F., *et al.*, *Nature* 306:234-238 (1983); Wexler, N.S., *et al.*, *Nature* 326:194-197 (1987)). Two other large families that have been described previously as Family Z and Family D, provided 25 and 35 HD chromosomes, respectively (Folstein, S.E., *et al.*, *Science* 229:776-779 (1985)). Normal chromosomes were taken from married-ins in the HD families and from unrelated normal individuals from non-HD families. The DNA tested for all individuals except four was prepared from lymphoblastoid cell lines or fresh blood (Gusella, J.F., *et al.*, *Nature* 306:234-238 (1983); Anderson and Gusella, *In Vitro* 20:856-858 (1984)). In the exceptional cases, DNA was prepared from frozen cerebellum. No difference in the characteristics of the PCR products were observed between lymphoblastoid, fresh blood, or brain DNAs. For five members of the Venezuelan pedigree aged 24-30, we also prepared DNA by extracting pelleted sperm from semen samples. The length of the HD gene (CAG)_n repeat for all DNAs was assessed using polymerase chain reaction amplification.

Statistical analysis as set forth in Examples 5-8. Associations between repeat lengths and onset age were assessed by Pearson correlation coefficient and by multivariate regression to assess higher order associations. Comparisons of the distributions of repeat length for all HD chromosomes and those for individual families were made by analysis of variance and t-test contrasts between groups. The 95 % confidence bands were computed around the regression line utilizing the general linear models procedure of SAS (SAS Institute Inc., SAS/STAT User's Guide, Version 6, Fourth Edition, Volume 2 (SAS Institute Inc., Cary, N.C., pp. 846, 1989)).

Example 1

Application of Exon Amplification to Obtain Trapped Cloned Exons

The HD candidate region defined by discrete recombination events in well-characterized families spans 2.2 Mb between D4S10 and D4S98 as shown in Figure 1. The 500 kb segment between D4S180 and D4S182 displays the strongest linkage disequilibrium with HD, with about 1/3 of disease chromosomes sharing a common haplotype, anchored by multi-allele polymorphisms at D4S127 and D4S95 (MacDonald *et al.*, *Nature Genet.* 1:99-103 (1992)). Sixty-four overlapping cosmids spanning about 480 kb from D4S180 to a location between D4S95 and D4S182 have been isolated by a combination of information from YAC (Baxendale *et al.*, *Nucleic Acids Res.* 19:6651 (1991)) and cosmid probe hybridization to high density filter grids of a chromosome 4 specific library, as well as additional libraries covering this region. Sixteen of these cosmids providing the complete contig are shown in Figure 1. We have previously used exon amplification to identify ADDA, the α -adducin locus, IT10C3, a novel putative transporter gene, and IT11, a novel G protein-coupled receptor kinase gene in the region distal to D4S127 (Figure 1).

Spliced together and is an efficient method of obtaining probes for screening cDNA libraries. Individual cosmids were processed, yielding 9 exon clones in the region from cosmids L134B9 to L181B10.

Two non-overlapping cDNAs were initially isolated using exon probes. IT15A was obtained by screening a transformed adult retinal cell cDNA library with exon clone DL118F5-U. IT16A was isolated by screening an adult frontal cortex cDNA library with a pool of three exon clones, DL83D3-8, DL83D3-1, and DL228B6-3. R. *et al.*, *Genomics* 10:103-110 (1991)). The cDNA libraries were screened by hybridizing the exon probes to the libraries. The cDNAs were then isolated by PCR amplification. The cDNAs were then sequenced and compared to the known sequence of the HD gene. The cDNAs were then used to screen a library of lymphoblastoid cell lines representing a normal individual and 2 independent tri-zygotes for HD chromosomes.

of different haplotypes. The same approximately 10-11 kb transcript was also detected in RNA from a variety of human tissues (liver, spleen, kidney, muscle and various regions of adult brain).

IT15A and IT16A were used to "walk" in a number of human tissue cDNA libraries in order to obtain the full-length transcript. Figure 3 shows a representation of 5 cDNA clones which define the IT15 transcript, under a schematic of the composite sequence derived as described in the legend. Figure 3 also displays the locations on the composite sequence of the 9 trapped exon clones.

The composite sequence of IT15, containing the entire predicted coding sequence, spans 10,366 bases including a tail of 18 A's as shown in Figure 4. An open reading frame of 9,432 bases begins with a potential initiator methionine codon at base 316, located in the context of an optimal translation initiation sequence. An in-frame stop codon is located 240 bases upstream from this site. The protein product of IT15 is predicted to be a 348 kDa protein containing 3,144 amino acids. Although the first Met codon in the long open reading frame has been chosen as the probably initiator codon, we cannot exclude that translation does not actually begin at a more 3' Met codon, producing a smaller protein.

Example 2

Polymorphic Variation of the (CAG)_n Trinucleotide Repeat

Near its 5' end, the IT15 sequence contains 21 copies of the triplet CAG, encoding glutamine (Figure 5). When this sequence was compared with genomic sequences that are known to surround simple sequence repeats (SSRs) in 4p16.3, it was found that normal cosmid L191F1 had 18 copies of the triplet indicating that the (CAG)_n repeat is polymorphic (Figure 5). Primers from the genomic sequence flanking the repeat were chosen to establish a PCR assay for this variation. In the normal population, this SSR polymorphism displays at least 17 discrete alleles (Table 1) ranging from about 11 to about 34 repeat units. Ninety-eight percent of the 173 normal chromosomes tested contained repeat lengths between 11 and 24 repeats. Two chromosomes were detected in the 25-30 repeat range and 2 normal chromosomes had 33 and 34 repeats respectively. The overall heterozygosity on normal chromosome was 80%. Based on sequence analysis of three clones, it appears that the variation is based entirely on the (CAG)_n, but the potential for variation of the smaller downstream (CCG)₇ which is also included in the PCR product, is also present.

Example 3

Instability of the Trinucleotide Repeat on HD chromosomes

Sequence analysis of cosmid GUST2-2130, derived from a chromosome with the major HD haplotype (see below), revealed 48 copies of the trinucleotide repeat, far greater than the largest normal allele (Figure 5). When the PCR assay was applied to HD chromosomes, a pattern strikingly different from the normal variation was observed. HD heterozygotes contained one discrete allelic product in the normal size range, and one PCR product of much larger size, suggesting that the (CAG)_n repeat on HD chromosomes is expanded relative to normal chromosomes.

Figure 6 shows the patterns observed when the PCR assay was performed on lymphoblast DNA from a selected nuclear family in a large Venezuelan HD kindred. In this family, DNA marker analysis has shown previously that the HD chromosome was transmitted from the father (lane 2) to seven children (lanes 3, 5, 6, 7, 8, 10 and 11). The three normal chromosomes present in this mating yielded a PCR product in the normal size range (AN1, AN2, AN3) that was inherited in a Mendelian fashion. The HD chromosome in the father yielded a diffuse, "fuzzy"-appearing PCR product slightly smaller than the 48 repeat product of the non-Venezuelan HD cosmid. Except for the DNA in lane 5 which did not PCR amplify and in lane 11 which displayed only a single normal allele, each of the affected children's DNA yielded a PCR product of different size. AF

products of progressively larger size. The absence of a HD-specific PCR product in lane 10 suggested that this child's DNA possessed a (CAG)_n repeat that was too long to amplify efficiently. This was verified by Southern blot analysis in which the expanded HD allele was easily detected and estimated to contain up to 100 copies of the repeat. Notably, this child had juvenile onset of HD at the very early age of 2 years. The onset of HD in the father was in his early 40s, typical of most adult HD patients in this population. The onset of HD in the mother was in her early 50s, also typical of most adult HD patients in this population. Keeping with this trend, the offspring represented in lane 6, with the fewest repeats remained asymptomatic.

when last examined at age of 30.

Figure 7 shows PCR analysis for a second sibship from the Venezuelan pedigree in which both parents are *HD* heterozygotes carrying the same *HD* chromosome based on DNA marker studies. Several of the offspring are *HD* homozygotes (lanes 6+7, 10+11, 13+14, 17+18, 23+24) as reported previously (Wexler *et al.*, *Nature* 326:194-197 (1987)). Each parent's DNA contained one allele in the normal range (AN1, AN2) which was transmitted in a Mendelian fashion. The *HD*-specific products (AE) from the DNA of both parents and children were all much larger than the normal allelic products and also showed extensive variation in mean size. A neurologic diagnosis for the offspring in this pedigree was not provided to maintain the blind status of investigators involved in the ongoing Venezuela *HD* project, although age of onset again appears to parallel repeat length. Paired samples under many of the individual symbols represent independent lymphoblast lines initiated at least one year apart. The variance between paired samples was not as great as between the different individuals, suggesting that the major differences in size of the PCR products resulted from meiotic transmission. Of special note is the result obtained in lanes 13 and 14. This *HD* homozygote's DNA yielded one PCR product larger and one smaller than the *HD*-specific PCR products of both parents.

To date, we have tested 75 independent *HD* families, representing all different reported in MacDonald *et al.*, *Nature Genet.* 1:99-103 (1992)) and a wide range of ethnic backgrounds. In all 75 cases, a PCR product larger than the normal size range was produced from the *HD* chromosome. The sizes of the *HD*-specific products ranged from 42 repeat copies to more than 66 copies, with a few individuals failing to yield a product because of the extreme length of the repeat. In these cases, Southern blot analysis revealed an increase in the length of an *EcoRI* fragment with the largest allele approximating 100 copies of the repeat. Figure 8 shows the variation detected in members of an American family of Irish ancestry in which the major *HD* haplotype is segregating. Cosmid GUS72-2130 was cloned from the *HD* homozygous individual whose DNA was amplified in lane 2. As was observed in the Venezuelan *HD* pedigree (Figures 6 and 7), which segregates the disorder with a different 4p16.3 haplotype, the *HD*-specific PCR products for this family display considerable size variation.

Example 4

New Mutations to *HD*

The mutation rate in *HD* has been reported to be very low. To test whether the expansion of the (CAG)_n repeat is the mechanism by which new *HD* mutations occur, two pedigrees with sporadic cases of *HD* have been examined in which intensive searching failed to reveal a family history of the disorder. In these cases, pedigree information sufficient to identify the same chromosomes in both the affected individual and unaffected relatives was gathered. Figures 9 and 10 show the results of PCR analysis of the (CAG)_n repeat in these families. The chromosomes in each family were assigned an arbitrary number based on typing for a large number of RFLP and SSR markers in 4p16.3 defining distinct haplotypes and the presumed *HD* chromosome is starred.

In family #1, *HD* first appeared in individual II-3 who transmitted the disorder to III-1 along with chromosome 3*. This same chromosome was present in II-2, an elderly unaffected individual. PCR analysis revealed that chromosome 3* from II-2 produced a PCR product at the extreme high end of the normal range (about 36 CAG copies). However, the (CAG)_n repeat on the same chromosome in II-3 and III-1 had undergone sequential expansions to about 44 and about 46 copies, respectively. A similar result was obtained in Family #2, where the presumed *HD* mutant III-2 had a considerably expanded repeat relative to the same chromosome in II-1 and III-1 (about 49 vs. about 33 CAG copies). In both family #1 and family #2, the ultimate *HD* chromosome displays the marker haplotype characteristic of 1/3 of all *HD* chromosomes, suggesting that this haplotype may be predisposed to undergoing repeat expansion.

These studies suggest that the (CAG)_n repeat is the mechanism by which new *HD* mutations occur. These results are consistent with the interpretation that *HD* constitutes the latest example of a mutational mechanism that may prove quite common in human genetic disease. Elongation of a trinucleotide repeat sequence has been implicated previously as the cause of three quite different human disorders, the fragile X syndrome, myotonic dystrophy and spino-bulbar muscular atrophy. The initial mechanism of repeat expansion in these disorders is not known, but it is likely that the same mechanism is involved in *HD*.

FIGURE 7. PCR analysis of DNA from a Venezuelan pedigree. The DNA of both parents and children were all much larger than the normal allelic products and also showed extensive variation in mean size.

a fragile site at Xq27.3 is associated with expansion of a (CGG)_n repeat thought to be in the 5' untranslated region of the *FMR1* gene (Fu *et al.*, *Cell* 67:1047-1058 (1991); Kremer *et al.*, *Science* 252:1711-1714 (1991); Verkerk *et al.*, *Cell* 65:904-914 (1991)). In myotonic dystrophy, a dominant disorder involving muscle weakness with myotonia that typically present in early adulthood, the unstable trinucleotide repeat, (CTG)_n, is located in the 3' untranslated region of the myotonic protein kinase gene (Aslanidis *et al.*, *Nature* 355:548-551 (1992); Brook *et al.*, *Cell* 68:799-808 (1992); Buxton *et al.*, *Nature* 355:547-548 (1992); Fu *et al.*, *Science* 255:1256-1259 (1992); Harley *et al.*, *Lancet* 339:1125-1128 (1992); Mahadevan *et al.*, *Science* 255:1253-1255 (1992)). The unstable (CAG)_n repeat in HD may be within the coding sequence of the IT15 gene, a feature shared with spino-bulbar muscular atrophy, an X-linked recessive adult-onset disorder of the motor neurons caused by expansion of a (CAG)_n repeat in the coding sequence of the androgen receptor gene (LaSpada *et al.*, *Nature* 352:77-79 (1991)). The repeat length in both the fragile X syndrome and myotonic dystrophy tends to increase in successive generations, sometimes quite dramatically. Occasionally, decreases in the average repeat length are observed (Fu *et al.*, *Science* 255:1256-1259 (1992); Yu *et al.*, *Am. J. Hum. Genet.* 50:968-980 (1992); Bruner *et al.*, *N. Engl. J. Med.* 327:476-480 (1992)). The HD trinucleotide repeat is also unstable, usually expanding when transmitted to the next generation, but contracting on occasion. In HD, as in the other disorders, change in copy number occurs in the absence of recombination. Compared with the fragile X syndrome, myotonic dystrophy, and HD, the instability of the disease allele in spino-bulbar muscular atrophy is more limited, and dramatic expansions of repeat length have not been seen (Biancalana *et al.*, *Hum. Mol. Genet.* 1:255-258 (1992)).

Expansion of the repeat length in myotonic dystrophy is associated with a particular chromosomal haplotype, suggesting the existence of a primordial predisposing mutation (Harley *et al.*, *Am. J. Hum. Genet.* 49:68-75 (1991); Harley *et al.*, *Nature* 355:545-546 (1992); Ashizawa, *Lancet* 338:642-643 (1991); and Epstein (1991)). In the fragile X syndrome, there may be a limited number of ancestral mutations that predispose to increases in trinucleotide repeat number (Richards *et al.*, *Nature Genet.* 1:257-260 (1992); Oudet *et al.*, *Am. J. Hum. Genet.* 52:297-304 (1993)). The linkage disequilibrium analysis used to identify IT15 indicates that there are several haplotypes associated with HD, but that at least 1/3 of HD chromosomes are ancestrally related (MacDonald *et al.*, *Nature Genet.* 1:99-103 (1992)). These data, combined with the reported low rate of new mutation to HD (Harper, *J. Med. Genet.* 89:365-376 (1992)), suggest that expansion of the trinucleotide repeat may only occur on select chromosomes. The analysis of two families presented herein, in which new mutation was supposed to have occurred, is consistent with the view that there may be particular normal chromosomes that have the capacity to undergo expansion of the repeat into the HD range. In each of these families, a chromosome with a (CAG)_n repeat length in the upper end of the normal range was segregating on a chromosome whose 4p16.3 haplotype matched the most common haplotype seen on HD chromosomes and the clinical appearance of HD in these two cases was associated with expansion of the trinucleotide repeat.

The recent application of haplotype analysis to explore the linkage disequilibrium on HD chromosomes pointed to a portion of a 2.2 Mb candidate region defined by the majority of recombination events described in HD pedigrees (MacDonald *et al.*, *Nature Genet.* 1:99-103 (1992)). Previously, the search for the gene was confounded by three matings in which the genetic inheritance pattern was inconsistent with the remainder of the family (MacDonald *et al.*, *Neuron* 3:183-190 (1989b); Prichard *et al.*, *Am. J. Hum. Genet.* 50:1218-1230 (1992)). These matings produced apparently affected HD individuals despite the inheritance of only normal alleles for markers throughout 4p16.3, effectively excluding inheritance of the HD chromosome present in the rest of the pedigree. Using PCR assay disclosed above, each of these families was tested and it was determined that like other HD kindreds, an expanded allele segregates with HD in affected individuals of all three pedigrees. However, an expanded allele was not present in those specific individuals with the inconsistent 4p16.3 genotypes. Instead, these individuals displayed the normal alleles expected based on analysis of other markers in 4p16.3. It is conceivable that these inconsistent individuals do not, in fact, have HD, but some other disorder. Alternatively, they might represent genetic mosaics in which the HD allele is more heavily represented and/or more expanded in brain tissue than in the lymphoblast DNA used for genotyping.

The capacity to monitor directly the size of the trinucleotide repeat in the DNA of lymphocytes in

individuals with or without affected relatives. However, it is of the utmost importance that the current internationally accepted guidelines and counseling protocols for testing those "at risk" continue to be observed, and that samples from unaffected relatives should not be tested inadvertently or without full consent. In the series of patients examined in this study, there is an apparent correlation between repeat length and age of onset

of the disease, reminiscent of that reported in myotonic dystrophy (Harley *et al.*, *Lancet* 339:1125-1128 (1992); Harley *et al.*, *Neuron* 3:183-190 (1989b); Prichard *et al.*, *Am. J. Hum. Genet.* 50:1218-1230 (1992)). This correlation is consistent with the hypothesis that the HD allele is more heavily represented and/or more expanded in brain tissue than in the lymphoblast DNA used for genotyping. (Amsterdam, pp. b45-b50 (1969)).

The expression of fragile X syndrome is associated with direct inactivation of the *FMR1* gene (Pierretti *et al.*, *Cell* 66:817-822 (1991); DeBouille *et al.*, *Nature Genet.* 3:31-35 (1993)). The recessive inheritance pattern of spino-bulbar muscular atrophy suggests that in this disorder, an inactive gene product is produced. In myo-

tonic dystrophy, the manner in which repeat expansion leads to the dominant disease phenotype is unknown. There are numerous possibilities for the mechanism of pathogenesis of the expanded trinucleotide repeat in HD. Without intending to be held to this theory, nevertheless notice can be taken that since Wolf-Hirschhorn patients hemizygous for 4p16.3 do not display features of HD, and IT15 mRNA is present in HD homozygotes, the expanded trinucleotide repeat does not cause simple inactivation of the gene containing it. The observation that the phenotype of HD is completely dominant, since homozygotes for the disease allele do not differ clinically from heterozygotes, has suggested that HD results from a gain of function mutation, in which either the mRNA product or the protein product of the disease allele would have some new property, or be expressed inappropriately (Wexler *et al.*, *Nature* 326:194-197 (1987); Myers *et al.*, *Am. J. Hum. Genet.* 45:615-618 (1989)). If the expanded trinucleotide repeat were translated, the consequences on the protein product would be dramatic, increasing the length of the poly-glutamine stretch near the N-terminus. It is possible, however, that despite the presence of an upstream Met codon, the normal translational start occurs 3' to the (CAG)_n repeat and there is no poly-glutamine stretch in the protein product. In this case, the repeat would be in the 5' untranslated region and might be expected to have its dominant effect at the mRNA level. The presence of an expanded repeat might directly alter regulation, localization, stability or translatability of the mRNA containing it, and could indirectly affect its counterpart from the normal allele in HD heterozygotes. Other conceivable scenarios are that the presence of an expanded repeat might alter the effective translation start site for the HD transcript, thereby truncating the protein, or alter the transcription start site for the IT15 gene, disrupting control of mRNA expression. Finally, although the repeat is located within the IT15 transcript, the possibility that it leads to HD by virtue of an action on the expression of an adjacent gene cannot be excluded.

Despite this final caveat, it is consistent with the above results and most likely that the trinucleotide repeat expansion causes HD by its effect, either at the mRNA or protein level, on the expression and/or structure of the protein product of the IT15 gene, which has been named huntingtin. Outside of the region of the triplet repeat, the IT15 DNA sequence detected no significant similarity to any previously reported gene in the GenBank database. Except for the stretches of glutamine and proline near the N-terminus, the amino acid sequence displayed no similarity to known proteins, providing no conspicuous clues to huntingtin's function. The poly-glutamine and poly-proline region near the N-terminus detect similarity with a large number of proteins which also contain long stretches of these amino acids. It is difficult to assess the significance of such similarities, although it is notable that many of these are DNA binding proteins and that huntingtin does have a single leucine zipper motif at residue 1,443. Huntingtin appears to be widely expressed, and yet cell death in HD is confined to specific neurons in particular regions of the brain.

TABLE 1. COMPARISON OF HD AND
NORMAL REPEAT SIZES

RANGE OF ALLELE SIZES (#REPEATS)	NORMAL CHROMOSOMES NUMBER AND FREQUENCY		HD CHROMOSOMES NUMBER AND FREQUENCY	
≥ 48	0	0	44	0.59
42-47	0	0	30	0.41
30-41	2	0.01	0	0
25-30	2	0.01	0	0
≤ 24	169	0.98	0	0
TOTAL	173	1.00	74	1.0

Example 5

Distribution of Trinucleotide Repeat Lengths on Normal and HD Chromosomes

The number of copies of the HD triplet repeat has been examined in a total of 425 HD chromosomes from 150 independent families and compared with the copy number of the HD triplet repeat of 545 normal chromosomes. The results are displayed in Figure 11. Two non-overlapping distributions of repeat length were observed, wherein the upper end of the normal range and the lower end of the HD range were separated by 3 repeat units. The normal chromosomes displayed 24 alleles producing PCR products ranging from 11 to 34 repeat units, with a median of 19 units (mean 19.71, s.d. 3.21). The HD chromosomes yielded 54 discrete PCR products corresponding to repeat lengths of 37 to 86 units, with a median of 45 units (mean 46.42, s.d. 6.68).

Of the HD chromosomes, 134 and 161 were known to be maternally or paternally-derived, respectively. To investigate whether the sex of the transmitting parent might influence the distribution of repeat lengths, these two sets of chromosomes were plotted separately in Figure 12. The maternally-derived chromosomes displayed repeat lengths ranging from 37 to 73 units, with a median of 44 (mean 44.93, s.d. 5.14). The paternally-derived chromosomes had 37 to 86 copies of the repeat unit, with a median of 48 units (mean 49.14, s.d. 8.27). However, a higher proportion of the paternally-derived HD chromosomes had repeat lengths greater than 55 units (16% vs. 2%), suggesting the possibility of a differential effect of paternal versus maternal transmission.

The data set used excluded chromosomes from a few clinically diagnosed individuals at the

These findings suggest that the pathogenesis of HD in individuals with low repeat length alleles and no clinical manifestations have not been explained, and they may represent phenocopies of HD. Regardless of the mechanism involved, the occurrence at low frequency of such individuals within known HD families must be considered if diagnostic conclusions are based solely on repeat length.

The control data set also excludes a number of chromosomes from phenotypically normal individuals who are related to 'sporadic' cases of EPL. For example, a family with two affected children and one unaffected child was excluded because the two affected children had identical bands for the marker on chromosome 12p13.3, and the unaffected child had a different band. This was done to avoid the possibility of a false-positive linkage signal. However, these exclusions were made after the initial analysis of the data, so that the data set they are essential the same chromosome

some as that of an affected relative, the diagnosed "spontaneous" HD proband, except with respect to repeat length. The lengths of repeat found on these ambiguous chromosomes (34-38 units) span the gap between the control and HD distributions, confounding a decision on the status of any individual with a repeat in the high normal to low HD range.

5

Example 6

Instability of the Trinucleotide Repeat

10 The data in Figure 11 combine repeat lengths from 150 different HD families representing many potentially independent origins of the defect. To examine the variation in repeat lengths on sets of HD chromosomes known to descend from a common founder, the data from three large HD kindreds (Gusella, J.F., *et al.*, *Nature* 306:234-238 (1983); Wexler, N.S., *et al.*, *Nature* 326:194-197 (1987); Folstein, S.E., *et al.*, *Science* 229:776-779 (1985)) with different 4p16.3 haplotypes (MacDonald, M.E., *et al.*, *Nature Genet.* 1:99-103 (1992)), typed for 75, 25 and 35 individuals, respectively, were separated. Despite the single origin of the founder HD chromosome with-
15 in each pedigree, members of the separate pedigrees display a wide range of repeat lengths (Figure 13). This instability of the HD chromosome repeat is most prominent in members of a large Venezuelan HD kindred (panel A) In which the common HD ancestor has produced 10 generations of descendants, numbering over 13,000 individuals. The distribution of repeat lengths in this sampling of the Venezuelan pedigree (median 46, mean 48.26, s.d. 9.3) is not significantly different from that of the larger sample of HD chromosomes from all families. Panels B and C display results for two extended families in which HD was introduced more recently than in the Venezuelan kindred. These families have been reported to exhibit different age of onset distributions and varied phenotypic features of HD (Folstein, S.E., *et al.*, *Science* 229:776-779 (1985)). Both revealed extensive repeat length variation, with a median of 41 and 49 repeat units, respectively. The distribution of repeat lengths
20 in the members of the family in Panel B was significantly different from the distribution of all HD chromosome repeat lengths ($p < 0.0001$), with a smaller mean of 42.04 repeat units (s.d. 2.82). The repeat distribution from HD chromosomes of Panel C was also significantly different from the total data set ($p < 0.004$), but with a higher mean of 49.80 (s.d. 5.86).

30 Example 7

Parental Source Effects on Repeat Length Variation

For 62 HD chromosomes in Figure 11, the length of the trinucleotide repeat also could be examined on
35 the corresponding parental HD chromosome. In 20 of 25 maternal transmissions, and in 31 of 37 paternal transmissions, the repeat length was altered, indicating considerable instability. A similar phenomenon was not observed for normal chromosomes, where more than 500 meiotic transmissions revealed no changes in repeat length, although the very existence of such a large number of normal alleles suggests at least a low degree of instability.

40 Figure 14 shows the relationship between the repeat lengths on the HD chromosomes in the affected parent and corresponding progeny. For the 20 maternally-inherited chromosomes on which the repeat length was altered, 13 changes were increases in length and 7 were decreases. Both increases and decreases involved changes of less than 5 repeat units and the overall correlation between the mother's repeat length and that of her child was $r = 0.95$ ($p < 0.0001$). The average change in repeat length in the 25 maternal transmissions was
45 an increase of 0.4 repeats.

On paternally-derived chromosomes, the 31 transmissions in which the repeat length changes comprised 26 length increases and 5 length decreases. Although the decreases in size were only slightly smaller than those observed on maternally-derived chromosomes, ranging from 1 to 3 repeat units, the average change of

1 repeat unit was observed. In one paternal transmission, the repeat length increased by 4 repeat units, a near doubling of the parental repeat.

For both male and female transmissions, there was no correlation between the size of the parental repeat and either the magnitude or frequency of changes.

55 To determine whether the variation in the length of the repeat observed through male transmission of HD chromosomes was attributable to a meiotic process, we examined the relationship between the repeat length of the sperm and the repeat length of the sperm's progeny. The relationship between the repeat length of the sperm and the repeat length of the sperm's progeny was examined for 10 sperm and 10 sperm's progeny. The relationship between the repeat length of the sperm and the repeat length of the sperm's progeny was examined for 10 sperm and 10 sperm's progeny. The relationship between the repeat length of the sperm and the repeat length of the sperm's progeny was examined for 10 sperm and 10 sperm's progeny.

the normal chromosome. All the sperm donors are members of the Venezuelan HD family and range in age from 24 to 30 years. Individuals 1 and 2 are siblings with HD chromosome repeat lengths based on lymphoblast DNA of 45 and 52, respectively. Individuals 3 and 4 are also siblings, with HD repeat lengths of 46 and 49, respectively. Individual 5, from a different sibship than either of the other two pairs, has an HD repeat of 52 copies. In all 5 cases, the PCR amplification of sperm DNA and lymphoblast DNA yielded identical products from the normal chromosome. However, in comparison with lymphoblast DNA, the HD gene from sperm DNA yielded a diffuse array of products. In 3 of the 5 cases (2,4 and 5), the diffuse array spread to much larger allelic products than the corresponding lymphoblast product. Subject 2 showed the greatest range of expansion, with the sperm DNA product extending to over 80 repeat units. Interestingly, the 3 individuals displaying the greatest variation have the longest repeats and are currently symptomatic. The other two donors have shorter repeat lengths in the HD range, and remain at risk at this time.

The striking difference in the high repeat length range (>55) between HD chromosomes transmitted from the father and those transmitted from the mother indicated a potential parental source effect. When this was examined directly, the HD chromosome repeat length changed in about 85% of transmissions. Most changes involved a fluctuation of only a few repeat units, with larger increases occurring only in male transmissions. The greater size increases in male transmission appear to be caused by particular instability of the HD trinucleotide repeat during male gametogenesis, based on the amplification of the repeat from sperm DNA.

Example 8

Relationship between Repeat Length and Age of Onset

Increased repeat length might correlate with a reduced age of onset of HD. Accordingly, age of onset data was determined for 234 of the individuals represented in Figure 11. Figure 16 displays the repeat lengths found on the HD and normal chromosomes of these individuals relative to their age of onset. Indeed, age of onset is inversely correlated with the HD repeat length. A Pearson correlation coefficient of $r=-.75$, $p<0.0001$ was obtained assuming a linear relationship between age of onset and repeat length. When a polynomial function was used, a better fit was obtained ($R^2=0.61$, $F=121.45$), suggesting a higher order association between age of onset and repeat length.

There is considerable variation in the age of onset associated with any specific number of repeat units, particularly for trinucleotide repeats in the 37-52 unit zone (88% of HD chromosomes) where onset ranged from 15 to 75 years. In this range, a linear relationship between age of onset and repeat length provided as good a fit as a higher order relationship. The 95 % confidence interval surrounding the predicted regression line was estimated at ± 18 years. In the 37 to 52 unit range, the association of repeat length to onset age is only half as strong as in the overall distribution ($r=-0.40$, $p<.0001$), indicating that much of the predictive power is contributed by repeats longer than 52 units. In this increased range, onset is likely to be very young and consequently not relevant to most persons seeking testing.

For the 178 cases in the 37-52 repeat unit range for which it was possible to subdivide the data set based on parental origin of the HD gene, multivariate regression analysis suggested a significant effect of parental origin on age of onset ($p<0.05$) independent of repeat length in this range. HD gene carriers from maternal transmissions had an average age of onset two years later than those from paternal transmissions.

In both univariate and multivariate analyses, no association between age of onset and the repeat length on the normal chromosome was detected, either in the total data set, or when it was subdivided into chromosomes of maternal or paternal origin.

All publications mentioned hereinabove are hereby incorporated in their entirety by reference.

While the foregoing invention has been described in some detail for purposes of clarity and understanding, it will be appreciated by one skilled in the art from a reading of this disclosure that various changes in form and detail can be made without departing from the spirit and scope of the invention.

SEQUENCE LISTING

- 5 (1) GENERAL INFORMATION:
- (i) APPLICANT: THE GENERAL HOSPITAL CORPORATION
Fruit Street
Boston, Massachusetts 02114
United States of America
- 10 (ii) TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
- 15 (A) KILBURN & STRODE
(B) 30 JOHN STREET
(C) LONDON
(D) GREAT BRITAIN
(E) WC1N 2DD
- 20 (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- 25 (vi) CURRENT APPLICATION DATA:
- (A) 7th March 1994
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- (A) APPLICATION NUMBER: 08/085,000
30 (B) FILING DATE: 01 JULY 1993
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- (A) APPLICATION NUMBER: 08/027,498
(B) FILING DATE: 05 MARCH 1993

35 (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCGGGAGAC CGCCATGGCG

20

45 (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs

ATAA GAGTAT A TATAG

17

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	Pro	Pro	Gly	Pro	Ala	Val	Ala	Glu	Glu	Pro	Leu	His	Arg	Pro	Lys	Lys	
				80					85					90			
5	GAA	CTT	TCA	GCT	ACC	AAG	AAA	GAC	CGT	GTG	AAT	CAT	TGT	CTG	ACA	ATA	639
	Glu	Leu	Ser	Ala	Thr	Lys	Lys	Asp	Arg	Val	Asn	His	Cys	Leu	Thr	Ile	
			95					100					105				
	TGT	GAA	AAC	ATA	GTG	GCA	CAG	TCT	GTG	AGA	AAT	TCT	CCA	GAA	TTT	CAG	687
	Cys	Glu	Asn	Ile	Val	Ala	Gln	Ser	Val	Arg	Asn	Ser	Pro	Glu	Phe	Gln	
		110					115					120					
10	AAA	CTT	CTG	GGC	ATC	GCT	ATG	GAA	CTT	TTT	CTG	CTG	TGC	AGT	GAT	GAC	735
	Lys	Leu	Leu	Gly	Ile	Ala	Met	Glu	Leu	Phe	Leu	Leu	Cys	Ser	Asp	Asp	
		125				130				135						140	
	GCA	GAC	TCA	CAT	CTC	ACC	ATC	CTG	GCT	GAC	GAA	TGC	CTC	AAC	AAA	GTT	783
15	Ala	Glu	Ser	Asp	Val	Arg	Met	Val	Ala	Asp	Glu	Cys	Leu	Asn	Lys	Val	
				145						150					155		
	ATC	AAA	GCT	TTG	ATG	GAT	TCT	AAT	CTT	CCA	AGG	TTA	CAG	CTC	GAG	CTC	831
	Ile	Lys	Ala	Leu	Met	Asp	Ser	Asn	Leu	Pro	Arg	Leu	Gln	Leu	Glu	Leu	
				160					165					170			
20	TAT	AAG	GAA	ATT	AAA	AAG	AAT	GGT	GCC	CCT	CGG	AGT	TTG	CGT	GCT	GCC	879
	Tyr	Lys	Glu	Ile	Lys	Lys	Asn	Gly	Ala	Pro	Arg	Ser	Leu	Arg	Ala	Ala	
			175					180						185			
	CTG	TGG	AGG	TTT	GCT	GAG	CTG	GCT	CAC	CTG	GTT	CGG	CCT	CAG	AAA	TGC	927
	Leu	Trp	Arg	Phe	Ala	Glu	Leu	Ala	His	Leu	Val	Arg	Pro	Gln	Lys	Cys	
		190					195					200					
25	AGG	CCT	TAC	CTG	GTG	AAC	CTT	CTG	CCG	TGC	CTG	ACT	CGA	ACA	AGC	AAG	975
	Arg	Pro	Tyr	Leu	Val	Asn	Leu	Leu	Pro	Cys	Leu	Thr	Arg	Thr	Ser	Lys	
		205				210					215					220	
	AGA	CCC	GAA	GAA	TCA	GTC	CAG	GAG	ACC	TTG	GCT	GCA	GCT	GTT	CCC	AAA	1023
30	Arg	Pro	Glu	Glu	Ser	Val	Gln	Glu	Thr	Leu	Ala	Ala	Ala	Val	Pro	Lys	
					225					230						235	
	ATT	ATG	GCT	TCT	TTT	GGC	AAT	TTT	GCA	AAT	GAC	AAT	GAA	ATT	AAG	GTT	1071
	Ile	Met	Ala	Ser	Phe	Gly	Asn	Phe	Ala	Asn	Asp	Asn	Glu	Ile	Lys	Val	
				240					245					250			
35	TTG	TTA	AAG	GCC	TTC	ATA	GCG	AAC	ETG	AAG	TCA	AGC	TCC	CCC	ACC	ATT	1119
	Leu	Leu	Lys	Ala	Phe	Ile	Ala	Asn	Leu	Lys	Ser	Ser	Ser	Pro	Thr	Ile	
			255					260					265				
	CGG	CGG	ACA	GCG	GCT	GGA	TCA	GCA	GTG	AGC	ATC	TGC	CAG	CAC	TCA	AGA	1167
	Arg	Arg	Thr	Ala	Ala	Gly	Ser	Ala	Val	Ser	Ile	Cys	Gln	His	Ser	Arg	
			270				275					280					
40	AGG	ACA	CAA	TAT	ITC	TAT	AGT	TGG	CTA	CTA	AAT	GTG	CTC	TTA	GGC	TTA	1215
	Arg	Thr	Gln	Tyr	Phe	Tyr	Ser	Prp	Leu	Leu	Asn	Val	Leu	Leu	Gly	Leu	
		285				290					295					300	
	CTC	GTT	CCT	GTC	GAG	GAT	GAA	CAC	TCC	ACT	CTG	CTG	ATT	CTT	GGC	GTG	1263
45	Leu	Val	Pro	Val	Glu	Asp	Glu	His	Ser	Thr	Leu	Leu	Ile	Leu	Gly	Val	
				305						310					315		
	CTG	CTC	ACC	CTG	AGG	TAT	TTG	GTG	CCC	CTG	CTG	CAG	CAG	CAG	GTG	AAG	1311
	TTT	CTT	CTT	CTT	CTT	CTT	CTT	CTT	CTT	CTT	CTT	CTT	CTT	CTT	CTT	CTT	1411
	Val	Ser	Ile	Pro	Ala	Val	Gln	Ile	Val	His	Val	Tyr	Ile	Leu	Thr	Leu	

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	365				370					375				380		
	CTG	TTG	CAG	CAG	CTC	TTC	AGA	ACG	CCT	CCA	CCC	GAG	CTT	CTG	CAA	ACC
5	Leu	Leu	Gln	Gln	Leu	Phe	Arg	Thr	Pro	Pro	Pro	Glu	Leu	Leu	Gln	Thr
					385					390					395	
	CTG	ACC	GCA	GTC	GGG	GGC	ATT	GGG	CAG	CTC	ACC	GCT	GCT	AAG	GAG	GAG
	Leu	Thr	Ala	Val	Gly	Gly	Ile	Gly	Gln	Leu	Thr	Ala	Ala	Lys	Glu	Glu
				400				405						410		
10	TCT	GGT	GGC	CGA	AGC	CGT	AGT	GGG	AGT	ATT	GTG	GAA	CTT	ATA	GCT	GGA
	Ser	Gly	Gly	Arg	Ser	Arg	Ser	Gly	Ser	Ile	Val	Glu	Leu	Ile	Ala	Gly
			415					420				425				
	GGG	GGT	TCC	TCA	TGC	AGC	CCT	GTC	CTT	TCA	AGA	AAA	CAA	AAA	GGC	AAA
15	Gly	Gly	Ser	Ser	Cys	Ser	Pro	Val	Leu	Ser	Arg	Lys	Gln	Lys	Gly	Lys
			430				435					440				
	GTG	CTC	TTA	GGA	GAA	GAA	GAA	GCC	TTG	GAG	GAT	GAC	TCT	GAA	TCG	AGA
	Val	Leu	Leu	Gly	Glu	Glu	Glu	Ala	Leu	Glu	Asp	Asp	Ser	Glu	Ser	Arg
	445					450					455					460
20	TCG	GAT	GTC	AGC	AGC	TCT	GCC	TTA	ACA	GCC	TCA	GTG	AAG	GAT	GAG	ATC
	Ser	Asp	Val	Ser	Ser	Ser	Ala	Leu	Thr	Ala	Ser	Val	Lys	Asp	Glu	Ile
				465					470					475		
	AGT	GGA	GAG	CTG	GCT	GCT	TCT	TCA	GGG	GTT	TCC	ACT	CCA	GGG	TCA	GCA
	Ser	Gly	Glu	Leu	Ala	Ala	Ser	Ser	Gly	Val	Ser	Thr	Pro	Gly	Ser	Ala
				480					485					490		
25	GGT	CAT	GAC	ATC	ATC	ACA	GAA	CAG	CCA	CGG	TCA	CAG	CAC	ACA	CTG	CAG
	Gly	His	Asp	Ile	Ile	Thr	Glu	Gln	Pro	Arg	Ser	Gln	His	Thr	Leu	Gln
			495				500						505			
	CGC	GAC	TCA	CTG	GAT	CTG	GCC	AGC	TGT	GAC	TTG	ACA	AGC	TCT	GCC	ACT
30	Ala	Asp	Ser	Leu	Asp	Leu	Ala	Ser	Cys	Asp	Leu	Thr	Ser	Ser	Ala	Thr
		510					515					520				
	GAT	GGG	GAT	GAG	GAG	GAT	ATC	TTG	AGC	CAC	AGC	TCC	AGC	CAG	GTC	AGC
	Asp	Gly	Asp	Glu	Glu	Asp	Ile	Leu	Ser	His	Ser	Ser	Ser	Gln	Val	Ser
	525					530					535					540
35	GCC	STC	CCA	TCT	GAC	CCT	GCC	ATG	GAC	CTG	AAT	GAT	GGG	ACC	CAG	GCC
	Ala	Val	Pro	Ser	Asp	Pro	Ala	Met	Asp	Leu	Asn	Asp	Gly	Thr	Gln	Ala
				545						550					555	
	TCG	TCG	CCC	ATC	AGC	GAC	AGC	TCC	CAG	ACC	ACC	ACC	CAA	GGG	CCT	GAT
	Ser	Ser	Pro	Ile	Ser	Asp	Ser	Ser	Gln	Thr	Thr	Thr	Glu	Gly	Pro	Asp
				560				565						570		
40	TCA	GCT	ATT	ACC	CCT	TCA	GAC	AGT	TCT	GAA	ATT	GTG	TTA	GAC	GGT	ACC
	Ser	Ala	Val	Thr	Pro	Ser	Asp	Ser	Ser	Glu	Ile	Val	Leu	Asp	Gly	Thr
			575					580					585			
	GAC	AAC	CAG	TAT	TTG	GGC	CTG	CAG	ATT	GGA	CAG	CCC	CAG	GAT	GAA	GAT
45	Asp	Asn	Gln	Tyr	Leu	Gly	Leu	Gln	Ile	Gly	Gln	Pro	Gln	Asp	Glu	Asp
		590					595					600				
	GAG	GAA	CCC	ACA	GCT	ATT	GTT	GCT	GAT	GAA	GGC	TCG	CAG	GGC	TTG	AGG
	TAT	TTT	ATG	AGT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT	TTT
55	His	Lys	Arg	Gln	Ile	Ser	Asp	Ser	Ser	Val	Asp	Lys	Ile	Val	Leu	Arg
				64												

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[illegible]

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	945	950	955	
5	AGA GAT CAA AGC AGT GTT TAC CTG AAA CTT CTC ATG CAT GAG ACG CAG Arg Asp Gln Ser Ser Val Tyr Leu Lys Leu Leu Met His Glu Thr Gln 960 965 970			3231
10	CCT CCA TCT CAT TTC TCC GTC AGC ACA ATA ACC AGA ATA TAT AGA GGC Pro Pro Ser His Phe Ser Val Ser Thr Ile Thr Arg Ile Tyr Arg Gly 975 980 985			3279
10	TAT AAC CTA CTA CCA AGC ATA ACA GAC GTC ACT ATG GAA AAT AAC CTT Tyr Asn Leu Leu Pro Ser Ile Thr Asp Val Thr Met Glu Asn Asn Leu 990 995 1000			3327
15	TCA AGA GTT ATT GCA GCA GTT TCT CAT GAA CTA ATC ACA TCA ACC ACC Ser Arg Val Ile Ala Ala Val Ser His Glu Leu Ile Thr Ser Thr Thr 1005 1010 1015 1020			3375
	AGA GCA CTC ACA TTT GGA TGC TGT GAA GCT TTG TGT CTT CTT TCC ACT Arg Ala Leu Thr Phe Gly Cys Cys Glu Ala Leu Cys Leu Leu Ser Thr 1025 1030 1035			3423
20	GCC TTC CCA GTT TGC ATT TGG AGT TTA GGT TGG CAC TGT GGA GTG CCT Ala Phe Pro Val Cys Ile Trp Ser Leu Gly Trp His Cys Gly Val Pro 1040 1045 1050			3471
25	CCA CTG AGT GCC TCA GAT GAG TCT AGG AAG AGC TGT ACC GTT GGG ATG Pro Leu Ser Ala Ser Asp Glu Ser Arg Lys Ser Cys Thr Val Gly Met 1055 1060 1065			3519
25	GCC ACA ATG ATT CTG ACC CTG CTC TCG TCA GCT TGG TTC CCA TTG GAT Ala Thr Met Ile Leu Thr Leu Leu Ser Ser Ala Trp Phe Pro Leu Asp 1070 1075 1080			3567
30	CTC TCA GCC CAT CAA GAT GCT TTG ATT TTG GCC GGA AAC TTG CTT GCA Leu Ser Ala His Gln Asp Ala Leu Ile Leu Ala Gly Asn Leu Leu Ala 1085 1090 1095 1100			3615
	GCC AGT GCT CCC AAA TCT CTG AGA AGT TCA TGG GCC TCT GAA GAA GAA Ala Ser Ala Pro Lys Ser Leu Arg Ser Ser Trp Ala Ser Glu Glu Glu 1105 1110 1115			3663
35	GCC AAC CCA GCA GCC ACC AAG CAA GAG GAG GTC TGG CCA GCC CTG GGG Ala Asn Pro Ala Ala Thr Lys Gln Glu Glu Val Trp Pro Ala Leu Gly 1120 1125 1130			3711
40	GAC CGG GCC CTG GTG CCC ATG GTG GAG CAG CTC TTC TCT CAC CTG CTG Asp Arg Ala Leu Val Pro Met Val Glu Gln Leu Phe Ser His Leu Leu 1135 1140 1145			3759
40	AAG CTC ATT AAC ATT TGT GCC CAG CTC CTG GAT GAC CTC GCT GCT GGA Lys Val Ile Asn Ile Cys Ala His Val Leu Asp Asp Val Ala Pro Gly 1150 1155 1160			3807
45	CCC GCA ATA AAG GCA GCC TTG CCT TCT CTA ACA AAC CCC CCT TCT CTA Pro Ala Ile Lys Ala Ala Leu Pro Ser Leu Thr Asn Pro Pro Ser Leu 1165 1170 1175 1180			3855
	AGT CCC ATC CGA CGA AAG GGG AAG GAG AAA GAA CCA GGA GAA CAA GCA Arg Leu Ile Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu 1185 1190 1195 1200			3903
55	AAA CAA CTT CAA CAA CCA CTT CTT CTT CTT CTT CTT CTT CTT CTT CTT Arg Ala Asp Arg Arg Thr Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260 1265 1270 1275 1280 1285 1290 1295 1300			4003

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	1230	1235	1240	
5	CTG AAA GCT ACA CAC GCT AAC TAC AAG GTC ACG CTG GAT CTT CAG AAC Leu Lys Ala Thr His Ala Asn Tyr Lys Val Thr Leu Asp Leu Gln Asn 1245 1250 1255 1260			4095
	AGC ACG GAA AAG TTT GGA GGG TTT CTC CGC TCA GCC TTG GAT GTT CTT Ser Thr Glu Lys Phe Gly Gly Phe Leu Arg Ser Ala Leu Asp Val Leu 1265 1270 1275			4143
10	TCT CAG ATA CTA GAG CTG GCC ACA CTG CAG GAC ATT GGG AAG TGT GTT Ser Gln Ile Leu Glu Leu Ala Thr Leu Gln Asp Ile Gly Lys Cys Val 1280 1285 1290			4191
15	GAA GAG ATC CTA GGA TAC CTG AAA TCC TGC TTT AGT CGA GAA CCA ATG Glu Glu Ile Leu Gly Tyr Leu Lys Ser Cys Phe Ser Arg Glu Pro Met 1295 1300 1305			4239
	ATG GCA ACT GTT TGT GTT CAA CAA TTG TTG AAG ACT CTC TTT GGC ACA Met Ala Thr Val Cys Val Gln Gln Leu Leu Lys Thr Leu Phe Gly Thr 1310 1315 1320			4287
20	AAC TTG GCC TCC CAG TTT GAT GGC TTA TCT TCC AAC CCC AGC AAG TCA Asn Leu Ala Ser Gln Phe Asp Gly Leu Ser Ser Asn Pro Ser Lys Ser 1325 1330 1335 1340			4335
	CAA GGC CGA GCA CAG CGC CTT GGC TCC TCC AGT GTG AGG CCA GGC TTG Gln Gly Arg Ala Gln Arg Leu Gly Ser Ser Val Arg Pro Gly Leu 1345 1350 1355			4383
25	TAC CAC TAC TGC TTC ATG GCC CCG TAC ACC CAC TTC ACC CAG GCC CTC Tyr His Tyr Cys Phe Met Ala Pro Tyr Thr His Phe Thr Gln Ala Leu 1360 1365 1370			4431
30	GCT GAC GCC AGC CTG AGG AAC ATG GTG CAG GCG GAG CAG GAG AAC GAC Ala Asp Ala Ser Leu Arg Asn Met Val Gln Ala Glu Gln Glu Asn Asp 1375 1380 1385			4479
	ACC TCG GGA TGG TTT GAT GTC CTC CAG AAA GTG TCT ACC CAG TTG AAG Thr Ser Gly Trp Phe Asp Val Leu Gln Lys Val Ser Thr Gln Leu Lys 1390 1395 1400			4527
35	ACA AAC CTC ACG AGT GTC ACA AAG AAC CGT GCA GAT AAG AAT GCT ATT Thr Asn Leu Thr Ser Val Thr Lys Asn Arg Ala Asp Lys Asn Ala Ile 1405 1410 1415 1420			4575
40	CAT AAT CAC ATT CGT TTG TTT GAA CCT CTT GTT ATA AAA GCT TTA AAA His Asn His Ile Arg Leu Phe Glu Pro Leu Val Ile Lys Ala Leu Lys 1425 1430 1435			4623
	CAG TAC ACG ACT ACA ACA TGT GTG CAG TTA CAG AAG CAG GTT TTA GAT Gln Tyr Thr Thr Thr Thr Cys Val Gln Leu Gln Lys Gln Val Leu Asp 1440 1445 1450			4671
45	TTG CTG GCG CAG CTG GTT CAG TTA CGG GTT AAT TAC TGT CTT CTG GAT Leu Leu Ala Gln Leu Val Gln Leu Arg Val Asn Tyr Cys Leu Leu Asp 1455 1460 1465			4719
	TCA GAT CAG GTG TTT ATT GGC TTT GTA TTG AAA CAG TTT GAA TAC ATT			4767
50	TTT TTT TTT TTA TTA TTA TTT TAT TAA TTT TAT TAT TTA AAA TAT ATC Phe Phe Leu Val Leu Leu Ser Tyr His Arg Tyr His Ser Lys Gln Ile			4863

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	1520	1525	1530	
5	GGA AGG AAG GCT GTG ACA CAT GCC ATA CCG GCT CTG CAG CCC ATA GTC Gly Arg Lys Ala Val Thr His Ala Ile Pro Ala Leu Gln Pro Ile Val 1535 1540 1545			4959
10	CAC GAC CTC TTT GTA TTA AGA GGA ACA AAT AAA GCT GAT GCA GGA AAA His Asp Leu Phe Val Leu Arg Gly Thr Asn Lys Ala Asp Ala Gly Lys 1550 1555 1560			5007
15	GAG CTT GAA ACC CAA AAA GAG GTG GTG GTG TCA ATG TTA CTG AGA CTC Glu Leu Glu Thr Gln Lys Glu Val Val Val Ser Met Leu Leu Arg Leu 1565 1570 1575 1580			5055
20	ATC CAG TAC CAT CAG GTG TTG GAG ATG TTC ATT CTT GTC CTG CAG CAG Ile Gln Tyr His Gln Val Leu Glu Met Phe Ile Leu Val Leu Gln Gln 1585 1590 1595			5103
25	TGC CAC AAG CAG AAT GAA GAC AAG TGG AAG CGA CTG TCT CGA CAG ATA Cys His Lys Glu Asn Glu Asp Lys Trp Lys Arg Leu Ser Arg Gln Ile 1600 1605 1610			5151
30	GCT GAC ATC ATC CTC CCA ATG TTA GCC AAA CAG CAG ATG CAC ATT GAC Ala Asp Ile Ile Leu Pro Met Leu Ala Lys Gln Gln Met His Ile Asp 1615 1620 1625			5199
35	TCT CAT GAA GCC CTT GGA GTG TTA AAT ACA TTA TTT GAG ATT TTG GCC Ser His Glu Ala Leu Gly Val Leu Asn Thr Leu Phe Glu Ile Leu Ala 1630 1635 1640			5247
40	CCT TCC TCC CTC CGT CCG GTA GAC ATG CTT TTA CGG AGT ATG TTC GTC Pro Ser Ser Leu Arg Pro Val Asp Met Leu Leu Arg Ser Met Phe Val 1645 1650 1655 1660			5295
45	ACT CCA AAC ACA ATG GCG TCC GTG AGC ACT GTT CAA CTG TGG ATA TCG Thr Pro Asn Thr Met Ala Ser Val Ser Thr Val Gln Leu Trp Ile Ser 1665 1670 1675			5343
50	GGA ATT CTG GCC ATT TTG AGG GTT CTG ATT TCC CAG TCA ACT GAA GAT Gly Ile Leu Ala Ile Leu Arg Val Leu Ile Ser Gln Ser Thr Glu Asp 1680 1685 1690			5391
55	ATT GTT CTT TCT CGT ATT CAG GAG CTC TCC TTC TCT CCG TAT TTA ATC Ile Val Leu Ser Arg Ile Gln Glu Leu Ser Phe Ser Pro Tyr Leu Ile 1695 1700 1705			5439
60	TCC TCT ACA GTA ATT AAT AGG TTA AGA GAT GGG GAC AGT ACT TCA ACG Ser Cys Thr Val Ile Asn Arg Leu Arg Asp Gly Asp Ser Thr Ser Thr 1710 1715 1720			5487
65	TTA GAA GAA CAC AGT GAA GCG AAA CAA ATA AAG AAT TTT CCA GAA GAA Leu Glu Glu His Ser Glu Gly Lys Gln Ile Lys Asn Leu Pro Glu Glu 1725 1730 1735 1740			5535
70	ACA TTT TCA AGG TTT CTA TTA CAA CTG GTT GGT ATT CTT TTA GAA GAC Thr Phe Ser Arg Phe Leu Leu Gln Leu Val Gly Ile Leu Leu Glu Asp 1745 1750 1755			5583
75	ATT CTT ACA AAA CAG CTG AAG GTG GAA ATG AGT GAG CAG CAA CAT AAT Ile Val Thr Lys Ile Leu Arg Thr Thr Thr Thr Thr Thr Thr Thr 1760 1765 1770 1775 1780 1785 1790 1795			5631
80	ATC AAT CTT TTA AAT TTA TTA TTA TTA TTA TTA TTA TTA TTA TTA TTA Ile Lys Thr Gly Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr 1795 1800 1805 1810 1815 1820 1825 1830 1835 1840 1845 1850			5679

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	1805		1810		1815		1820	
5	AAC TTG CGG GCT CGT TCC ATG ATC ACC ACC CAC CCG GCC CTG GTG CTG		Asn Leu Arg Ala Arg Ser Met Ile Thr Thr His Pro Ala Leu Val Leu		5823			
			1825		1830		1835	
	CTC TGG TGT CAG ATA CTG CTG CTT GTC AAC CAC ACC GAC TAC CGC TGG		Leu Trp Cys Gln Ile Leu Leu Leu Val Asn His Thr Asp Tyr Arg Trp		5871			
			1840		1845		1850	
10	TGG GCA GAA GTG CAG CAG ACC CCG AAA AGA CAC AGT CTG TCC AGC ACA		Trp Ala Glu Val Gln Gln Thr Pro Lys Arg His Ser Leu Ser Ser Thr		5919			
			1855		1860		1865	
	AAG TTA CTT AGT CCC CAG ATG TCT GGA GAA GAG GAG GAT TCT GAC TTG		Lys Leu Leu Ser Pro Gln Met Ser Gly Glu Glu Glu Asp Ser Asp Leu		5967			
15			1870		1875		1880	
	GCA GCC AAA CTT GGA ATG TGC AAT AGA GAA ATA GTA CGA AGA GGG GCT		Ala Ala Lys Leu Gly Met Cys Asn Arg Glu Ile Val Arg Arg Gly Ala		6015			
			1885		1890		1895	
20	CTC ATT CTC TTC TGT GAT TAT GTC TGT CAG AAC CTC CAT GAC TCC GAG		Leu Ile Leu Phe Cys Asp Tyr Val Cys Gln Asn Leu His Asp Ser Glu		6063			
			1905		1910		1915	
	CAC TTA ACG TGG CTC ATT GTA AAT CAC ATT CAA GAT CTG ATC AGC CTT		His Leu Thr Trp Leu Ile Val Asn His Ile Gln Asp Leu Ile Ser Leu		6111			
			1920		1925		1930	
25	TCC CAC GAG CCT CCA GTA CAG GAC TTC ATC AGT GCC GTT CAT CGG AAC		Ser His Glu Pro Pro Val Gln Asp Phe Ile Ser Ala Val His Arg Asn		6159			
			1935		1940		1945	
	TCT GCT GCC AGC GGC CTG TTC ATC CAG GCA ATT CAG TCT CGT TGT GAA		Ser Ala Ala Ser Gly Leu Phe Ile Gln Ala Ile Gln Ser Arg Cys Glu		6207			
30			1950		1955		1960	
	AAC CTT TCA ACT CCA ACC ATG CTG AAG AAA ACT CTT CAG TGC TTG GAG		Asn Leu Ser Thr Pro Thr Met Leu Lys Lys Thr Leu Gln Cys Leu Glu		6255			
			1965		1970		1975	
35	GGG ATC CAT CTC AGC CAG TCG GGA GCT GTG CTC ACG CTG TAT GTG GAC		Gly Ile His Leu Ser Gln Ser Gly Ala Val Leu Thr Leu Tyr Val Asp		6303			
			1985		1990		1995	
	AGG CTT CTG TGC ACC CCT TTC GGT GIG CTG GCT CGC ATG GTC GAC ATC		Arg Leu Leu Cys Thr Pro Phe Arg Val Leu Ala Arg Met Val Asp Ile		6351			
40			2000		2005		2010	
	CTT GCT TGT GGC CGG GTA GAA ATG GTT CTG GCT GCA AAT TTA CAG AGC		Leu Ala Cys Arg Arg Val Glu Met Leu Leu Ala Ala Asn Leu Gln Ser		6399			
			2015		2020		2025	
45	AGC ATG GCC CAG TTG CCA ATG GAA GAA CTC AAC AGA ATC CAG GAA TAC		Ser Met Ala Gln Leu Pro Met Glu Glu Leu Asn Arg Ile Gln Glu Tyr		6447			
			2030		2035		2040	
	CTT CAG AGC AGC GGG CTC GCT CAG AGA CAG TAA AGG CTC TAT TCG CTG							6495
55	CTT CAA ATT CTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT		Pro Pro Val Ser Ser His Leu Leu Asp Gly Asp Gly His Val Ser Leu		6541			

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	2095	2100	2105	
5	CAG TGT TGG ACC AGG TCA GAT TCT GCA CTG CTG GAA GGT GCA GAG CTG Gln Cys Trp Thr Arg Ser Asp Ser Ala Leu Leu Glu Gly Ala Glu Leu 2110 2115 2120			5687
	GTG AAT CGG ATT CCT GCT GAA GAT ATG AAT GCC TTC ATG ATG AAC TCG Val Asn Arg Ile Pro Ala Glu Asp Met Asn Ala Phe Met Met Asn Ser 2125 2130 2135 2140			5735
10	GAG TTC AAC CTA AGC CTG CTA GCT CCA TGC TTA AGC CTA GGG ATG AGT Glu Phe Asn Leu Ser Leu Leu Ala Pro Cys Leu Ser Leu Gly Met Ser 2145 2150 2155			5783
	GAA ATT TCT GGT GGC CAG AAG AGT GCC CTT TTT GAA GCA GCC CGT GAG Glu Ile Ser Gly Gly Gln Lys Ser Ala Leu Phe Glu Ala Ala Arg Glu 2160 2165 2170			5831
15	GTG ACT CTG GCC CGT GTG AGC GGC ACC GTG CAG CAG CTC CCT GCT GTC Val Thr Leu Ala Arg Val Ser Gly Thr Val Gln Gln Leu Pro Ala Val 2175 2180 2185			5879
20	CAT CAT GTC TTC CAG CCC GAG CTG CCT GCA GAG CCG GCG GCC TAC TGG His His Val Phe Gln Pro Glu Leu Pro Ala Glu Pro Ala Ala Tyr Trp 2190 2195 2200			5927
	AGC AAG TTG AAT GAT CTG TTT GGG GAT GCT GCA CTG TAT CAG TCC CTG Ser Lys Leu Asn Asp Leu Phe Gly Asp Ala Ala Leu Tyr Gln Ser Leu 2205 2210 2215 2220			5975
25	CCC ACT CTG GCC CGG GCC CTG GCA CAG TAC CTG GTG GTG GTC TCC AAA Pro Thr Leu Ala Arg Ala Leu Ala Gln Tyr Leu Val Val Val Ser Lys 2225 2230 2235			7023
30	CTG CCC AGT CAT TTG CAC CTT CCT CCT GAG AAA GAG AAG GAC ATT GTG Leu Pro Ser His Leu His Leu Pro Pro Glu Lys Glu Lys Asp Ile Val 2240 2245 2250			7071
	AAA TTC GTG GTG GCA ACC CTT GAG GCC CTG TCC TGG CAT TTG ATC CAT Lys Phe Val Val Ala Thr Leu Glu Ala Leu Ser Trp His Leu Ile His 2255 2260 2265			7119
35	GAG CAG ATC CCG CTG AGT CTG GAT CTC CAG GCA GGG CTG GAC TGC TGC Glu Gln Ile Pro Leu Ser Leu Asp Leu Gln Ala Gly Leu Asp Cys Cys 2270 2275 2280			7167
40	TGC CTG GGC CTG CAG CTG CCT GGC CTC TGG AGC GTG GTC TCC TCC ACA Cys Leu Ala Leu Gln Leu Pro Gly Leu Trp Ser Val Val Ser Ser Thr 2285 2290 2295 2300			7215
	JAG TTT GTG ACC GAG GGC TGC TGC CTC ATC TAC TGT GTG CAC TTC ATC Glu Phe Val Thr His Ala Cys Ser Leu Ile Tyr Cys Val His Phe Ile 2305 2310 2315			7263
45	CTG GAG GCC GTT GCA GTG CAG CCT GGA GAG CAG CTT CTT AGT CCA GAA Leu Glu Ala Val Ala Val Gln Pro Gly Glu Gln Leu Leu Ser Pro Glu 2320 2325 2330			7311
	AGA AGG ACA AAT ACC CCA AAA GCC ATC AGC GAG GAG GAG GAG GAA GTA 2335 2340 2345 2350 2355 2360			7359
55	CTG GAA AAA ATG TTA GAT TTT CTA TAA TTA TTA TTA TTA TTA TTA TTA Val Ala Glu Met Val Glu Ser Leu Glu Ser Val Leu Ala Leu His His 2365 2370 2375 2380 2385 2390 2395 2400			7411

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	2385	2390	2395	
5	ATC ATC ATC AGC CTG GCC CGC CTG CCC CTT GTC AAC AGC TAC ACA CGT Ile Ile Ile Ser Leu Ala Arg Leu Pro Leu Val Asn Ser Tyr Thr Arg 2400 2405 2410			7551
10	GTG CCC CCA CTG GTG TGG AAG CTT GGA TGG TCA CCC AAA CCG GGA GGG Val Pro Pro Leu Val Trp Lys Leu Gly Trp Ser Pro Lys Pro Gly Gly 2415 2420 2425			7599
15	GAT TTT GGC ACA GCA TTC CCT GAG ATC CCC GTG GAG TTC CTC CAG GAA Asp Phe Gly Thr Ala Phe Pro Glu Ile Pro Val Glu Phe Leu Gln Glu 2430 2435 2440			7647
20	AAG GAA GTC TTT AAG GAG TTC ATC TAC CGC ATC AAC ACA CTA GGC TGG Lys Glu Val Phe Lys Glu Phe Ile Tyr Arg Ile Asn Thr Leu Gly Trp 2445 2450 2455 2460			7695
25	ACC AGT CGT ACT CAG TTT GAA GAA ACT TGG GCC ACC CTC CTT GGT GTC Thr Ser Arg Thr Gln Phe Glu Glu Thr Trp Ala Thr Leu Leu Gly Val 2465 2470 2475			7743
30	CTG GTG ACG CAG CCC CTC GTG ATG GAG CAG GAG GAG AGC CCA CCA GAA Leu Val Thr Gln Pro Leu Val Met Glu Gln Glu Glu Ser Pro Pro Glu 2480 2485 2490			7791
35	GAA GAC ACA GAG AGG ACC CAG ATC AAC GTC CTG GCC GTG CAG GCC ATC Glu Asp Thr Glu Arg Thr Gln Ile Asn Val Leu Ala Val Gln Ala Ile 2495 2500 2505			7839
40	ACC TCA CTG GTG CTC AGT GCA ATG ACT GTG CCT GTG GCC GGC AAC CCA Thr Ser Leu Val Leu Ser Ala Met Thr Val Pro Val Ala Gly Asn Pro 2510 2515 2520			7887
45	GCT GTA AGC TGC TTG GAG CAG CAG CCC CGG AAC AAG CCT CTG AAA GCT Ala Val Ser Cys Leu Glu Gln Gln Pro Arg Asn Lys Pro Leu Lys Ala 2525 2530 2535 2540			7935
50	CTC GAC ACC AGG TTT GGG AGG AAG CTG AGC ATT ATC AGA GGG ATT GTG Leu Asp Thr Arg Phe Gly Arg Lys Leu Ser Ile Ile Arg Gly Ile Val 2545 2550 2555			7983
55	GAG CAA GAG ATT CAA GCA ATG GTT TCA AAG AGA GAG AAT ATT GCC ACC Glu Gln Glu Ile Gln Ala Met Val Ser Lys Arg Glu Asn Ile Ala Thr 2560 2565 2570			8031
60	CAT CAT TTA TAT CAG GCA TGG CAT CCT GTC CCT TCT CTG TCT CCG GCT His His Leu Tyr Gln Ala Trp Asp Pro Val Pro Ser Leu Ser Pro Ala 2575 2580 2585			8079
65	ACT ACA GGT GCC CTC ATC AGC CAG CAG AAG CTG CTG CTA CAG ATC AAC Thr Thr Gly Ala Leu Ile Ser His Glu Lys Leu Leu Leu Gln Ile Asn 2590 2595 2600			8127
70	CCC GAG CGG GAG CTG GGG AGC ATG AGC TAC AAA CTC GGC CAG GTG TCC Pro Glu Arg Glu Leu Gly Ser Met Ser Tyr Lys Leu Gly Gln Val Ser 2605 2610 2615 2620			8175
75	ATA CAC TCC GTG TGG CTG GGG AAC AGC ATC ACA CCC CTG AGG GAG GAG Ile His Pro Thr Thr Val Val Val Val Val Val Val Val Val Val Val Val 2625 2630 2635 2640 2645 2650 2655 2660 2665 2670 2675 2680			8223
80	ATA CAC TCC GTG TGG CTG GGG AAC AGC ATC ACA CCC CTG AGG GAG GAG Ile His Pro Thr Thr Val Val Val Val Val Val Val Val Val Val Val Val 2685 2690 2695 2700 2705 2710 2715 2720 2725 2730 2735 2740			8317

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	2670	2675	2680	
5	ATC CTG CCG TCC AGC TCA GCC AGG AGG ACC CCG GCC ATC CTG ATC AGT Ile Leu Pro Ser Ser Ser Ala Arg Arg Thr Pro Ala Ile Leu Ile Ser 2685 2690 2695 2700	8415		
10	GAG GTG GTC AGA TCC CTT CTA GTG GTC TCA GAC TTG TTC ACC GAG CGC Glu Val Val Arg Ser Leu Leu Val Val Ser Asp Leu Phe Thr Glu Arg 2705 2710 2715	8463		
15	AAC CAG TTT GAG CTG ATG TAT GTG ACG CTG ACA GAA CTG CGA AGG GTG Asn Gln Phe Glu Leu Met Tyr Val Thr Leu Thr Glu Leu Arg Arg Val 2720 2725 2730	8511		
20	CAC CCT TCA GAA GAC GAG ATC CTC GCT CAG TAC CTG GTG CCT GCC ACC His Pro Ser Glu Asp Glu Ile Leu Ala Gln Tyr Leu Val Pro Ala Thr 2735 2740 2745	8559		
25	TGC AAG GCA GCT GCC GTC CTT GGG ATG GAC AAG GCC GTG GCG GAG CCT Cys Lys Ala Ala Ala Val Leu Gly Met Asp Lys Ala Val Ala Glu Pro 2750 2755 2760	8607		
30	GTC AGC CGC CTG CTG GAG AGC ACG CTC AGG AGC AGC CAC CTG CCC AGC Val Ser Arg Leu Leu Glu Ser Thr Leu Arg Ser Ser His Leu Pro Ser 2765 2770 2775 2780	8655		
35	AGG GTT GGA GCC CTG CAC CGC ATC CTC TAT GTG CTG GAG TGC GAC CTG Arg Val Gly Ala Leu His Gly Ile Leu Tyr Val Leu Glu Cys Asp Leu 2785 2790 2795	8703		
40	CTG GAC GAC ACT GCC AAG CAG CTC ATC CCG GTC ATC AGC GAC TAT CTC Leu Asp Asp Thr Ala Lys Gln Leu Ile Pro Val Ile Ser Asp Tyr Leu 2800 2805 2810	8751		
45	CTC TCC AAC CTG AAA GGG ATC GCC CAC TGC GTG AAC ATT CAC AGC CAG Leu Ser Asn Leu Lys Gly Ile Ala His Cys Val Asn Ile His Ser Gln 2815 2820 2825	8799		
50	CAG CAC GTA CTG GTC ATG TGT GCC ACT GCG TTT TAC CTC ATT GAG AAC Gln His Val Leu Val Met Cys Ala Thr Ala Phe Tyr Leu Ile Glu Asn 2830 2835 2840	8847		
55	TAT CCT CTG GAC GTA GGG CCG GAA TTT TCA GCA TCA ATA ATA CAG ATG Tyr Pro Leu Asp Val Gly Pro Glu Phe Ser Ala Ser Ile Ile Gln Met 2845 2850 2855 2860	8895		
60	ACT GGG GTG ATG CTG TCT GGA AGT GAG GAG TCC ACC CCC TCC ATC ATT Cys Gly Val Met Leu Ser Gly Ser Glu Glu Ser Thr Pro Ser Ile Ile 2865 2870 2875	8943		
65	TAC CAC TGT GCG CTC AGA GGC ATG GAG TCG CTC CTC CTC TCT GAG CAG Tyr His Cys Ala Leu Arg Gly Leu Glu Arg Leu Leu Leu Ser Glu Gln 2880 2885 2890	8991		
70	CTC TCC CGC CTG GAT GCA GAA TCG CTG GTC AAG CTG AGT GTG GAC AGA Leu Ser Arg Leu Asp Ala Glu Ser Leu Val Lys Leu Ser Val Asp Arg 2895 2900 2905	9039		
75	GTG AAC GTG CAC AGC CCG CAC CCG GCG ATG GCG GCT CTG GGC CTG ATG Val Asn Val His Ser Pro His Arg Ala Met Ala Ala Thr Ala Thr Ala 2910 2915 2920 2925 2930 2935	9087		
80	CTA GAT GAT AAT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT Gln Asp Phe Asn Ile Ala Ala Ile Arg Pro Ile Thr Ser Ile Thr Ala 2940 2945 2950 2955 2960 2965 2970 2975 2980 2985	9135		

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	2960	2965	2970	
5	TGT GAA GCC AGA GTG GTG GCC AGG ATC CTG CCC CAG TTT CTA GAC GAC Cys Glu Ala Arg Val Val Ala Arg Ile Leu Pro Gln Phe Leu Asp Asp 2975 2980 2985			9279
	TTC TTC CCA CCC CAG GAC ATC ATG AAC AAA GTC ATC GGA GAG TTT CTG Phe Phe Pro Pro Gln Asp Ile Met Asn Lys Val Ile Gly Glu Phe Leu 2990 2995 3000			9327
10	TCC AAC CAG CAG CCA TAC CCC CAG TTC ATG GCC ACC GTG GTG TAT AAG Ser Asn Gln Gln Pro Tyr Pro Gln Phe Met Ala Thr Val Val Tyr Lys 3005 3010 3015 3020			9375
15	GTG TTT CAG ACT CTG CAC AGC ACC GGG CAG TCG TCC ATG GTC CGG GAC Val Phe Gln Thr Leu His Ser Thr Gly Gln Ser Ser Met Val Arg Asp 3025 3030 3035			9423
	TGG GTC ATG CTG TCC CTC TCC AAC TTC ACG CAG AGG GCC CCG GTC GCC Trp Val Met Leu Ser Leu Ser Asn Phe Thr Gln Arg Ala Pro Val Ala 3040 3045 3050			9471
20	ATG GCC ACG TGG AGC CTC TCC TGC TTC TTT GTC AGC GCG TCC ACC AGC Met Ala Thr Trp Ser Leu Ser Cys Phe Phe Val Ser Ala Ser Thr Ser 3055 3060 3065			9519
	CCG TGG GTC GCG GCG ATC CTC CCA CAT GTC ATC AGC AGG ATG GGC AAG Pro Trp Val Ala Ala Ile Leu Pro His Val Ile Ser Arg Met Gly Lys 3070 3075 3080			9567
25	CTG GAG CAG GTG GAC GTG AAC CTT TTC TGC CTG GTC GCC ACA GAC TTC Leu Glu Gln Val Asp Val Asn Leu Phe Cys Leu Val Ala Thr Asp Phe 3085 3090 3095 3100			9615
30	TAC AGA CAC CAG ATA GAG GAG GAG CTC GAC CGC AGG GCC TTC CAG TCT Tyr Arg His Gln Ile Glu Glu Glu Leu Asp Arg Arg Ala Phe Gln Ser 3105 3110 3115			9663
	GTG CTT GAG GTG GTT GCA GCC CCA GGA AGC CCA TAT CAC CGG CTG CTG Val Leu Glu Val Val Ala Ala Pro Gly Ser Pro Tyr His Arg Leu Leu 3120 3125 3130			9711
35	ACT TGT TTA CGA AAT GTC CAC AAG GTC ACC ACC TCC T GAGCGCCATG Thr Cys Leu Arg Asn Val His Lys Val Thr Thr Cys 3135 3140			9758
	GTGGGAGAGA CTGTGAGGCG GCAGCTGGGG CCGGAGCCTT TGGAAAGTCTG TGCCCTTGTG			9818
40	CCCTGCTTCC ACUGAGCCAG CTTGGTCCCT ATGGGCTTCC GCACATGCCG CCGGCGGCCA			9878
	CGCAACGTGC GTGTCTCTGC CATGTGGTAA AATGTCTCTT TGTTGGCASTG GCGAGGCAGG			9938
	GAGTGTCTGC AGTCCTGGTG GGGCTGAGCC TGAGGCGCTT CAGAAAGCAG GAGCAGCTGT			9998
45	GCTGCACCCC ATGTGGGTGA CCAGGTCCTT TCTCCTGATA GTCACCTGCT GGTGTGTTGCC			10058
	AGGTTGCAGC TGCTCTTGCA TCTGGGCTAG AAGTCTCTCC TCCTGCAGGC TGGCTGTGCG			10118
	CCCTCTCTGT GTCTGTCAST AGAAGGTGCC GTGAGCAGGC TTTGGGAACA CTGGCCTGGG			10178

AAAAAAAA

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(A) LENGTH: 3144 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

5 Met Ala Thr Leu Glu Lys Leu Met Lys Ala Phe Glu Ser Leu Lys Ser
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10 Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
20 25 30

Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro Pro
35 40 45

15 Pro Pro Pro Gln Leu Pro Gln Pro Pro Pro Gln Ala Gln Pro Leu Leu
50 55 60

Pro Gln Pro Gln Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Gly Pro
65 70 75 80

20 Ala Val Ala Glu Glu Pro Leu His Arg Pro Lys Lys Glu Leu Ser Ala
85 90 95

Thr Lys Lys Asp Arg Val Asn His Cys Leu Thr Ile Cys Glu Asn Ile
100 105 110

25 Val Ala Gln Ser Val Arg Asn Ser Pro Glu Phe Gln Lys Leu Leu Gly
115 120 125

Ile Ala Met Glu Leu Phe Leu Leu Cys Ser Asp Asp Ala Glu Ser Asp
130 135 140

30 Val Arg Met Val Ala Asp Glu Cys Leu Asn Lys Val Ile Lys Ala Leu
145 150 155 160

Met Asp Ser Asn Leu Pro Arg Leu Gln Leu Glu Leu Tyr Lys Glu Ile
165 170 175

35 Lys Lys Asn Gly Ala Pro Arg Ser Leu Arg Ala Ala Leu Trp Arg Phe
180 185 190

Ala Glu Leu Ala His Leu Val Arg Pro Gln Lys Cys Arg Pro Tyr Leu
195 200 205

40 Val Asn Leu Leu Pro Cys Leu Thr Arg Thr Ser Lys Arg Pro Glu Glu
210 215 220

Ser Val Gln Glu Thr Leu Ala Ala Ala Val Pro Lys Ile Met Ala Ser
225 230 235 240

Phe Gly Asn Phe Ala Asn Asp Asn Glu Ile Lys Val Leu Leu Lys Ala
245 250 255

45 Phe Ile Ala Asn Leu Lys Ser Ser Ser Pro Thr Ile Arg Arg Thr Ala
260 265 270

55 Arg Thr Ser Val Pro Leu Leu Leu His His His Val Ser Asp Thr Ser Leu

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	Ala Glu Gln Leu Val Gln Val Tyr Glu Leu Thr Leu His His Thr Gln 355 360 365		
5	His Gln Asp His Asn Val Val Thr Gly Ala Leu Glu Leu Leu Gln Gln 370 375 380		
	Leu Phe Arg Thr Pro Pro Pro Glu Leu Leu Gln Thr Leu Thr Ala Val 385 390 395 400		
10	Gly Gly Ile Gly Gln Leu Thr Ala Ala Lys Glu Glu Ser Gly Gly Arg 405 410 415		
	Ser Arg Ser Gly Ser Ile Val Glu Leu Ile Ala Gly Gly Gly Ser Ser 420 425 430		
15	Cys Ser Pro Val Leu Ser Arg Lys Gln Lys Gly Lys Val Leu Leu Gly 435 440 445		
	Glu Glu Glu Ala Leu Glu Asp Asp Ser Glu Ser Arg Ser Asp Val Ser 450 455 460		
20	Ser Ser Ala Leu Thr Ala Ser Val Lys Asp Glu Ile Ser Gly Glu Leu 465 470 475 480		
	Ala Ala Ser Ser Gly Val Ser Thr Pro Gly Ser Ala Gly His Asp Ile 485 490 495		
25	Ile Thr Glu Gln Pro Arg Ser Gln His Thr Leu Gln Ala Asp Ser Leu 500 505 510		
	Asp Leu Ala Ser Cys Asp Leu Thr Ser Ser Ala Thr Asp Gly Asp Glu 515 520 525		
30	Glu Asp Ile Leu Ser His Ser Ser Ser Gln Val Ser Ala Val Pro Ser 530 535 540		
	Asp Pro Ala Met Asp Leu Asn Asp Gly Thr Gln Ala Ser Ser Pro Ile 545 550 555 560		
35	Ser Asp Ser Ser Gln Thr Thr Thr Glu Gly Pro Asp Ser Ala Val Thr 565 570 575		
	Pro Ser Asp Ser Ser Glu Ile Val Leu Asp Gly Thr Asp Asn Gln Tyr 580 585 590		
40	Leu Gly Leu Gln Ile Gly Gln Pro Gln Asp Glu Asp Glu Glu Ala Thr 595 600 605		
	Gly Ile Leu Pro Asp Glu Ala Ser Glu Ala Phe Arg Asn Ser Ser Met 610 615 620		
45	Ala Leu Gln Gln Ala His Leu Leu Lys Asn Met Ser His Cys Arg Gln 625 630 635 640		
	Pro Ser Asp Ser Ser Val Asp Lys Phe Val Leu Arg Asp Glu Ala Thr 645 650 655		
50	Pro Ser Asp Ser Ser Val Asp Lys Phe Val Leu Arg Asp Glu Ala Thr 660 665 670		
55	Pro Ser Asp Ser Ser Val Asp Lys Phe Val Leu Arg Asp Glu Ala Thr 675 680 685		
60	Pro Ser Asp Ser Ser Val Asp Lys Phe Val Leu Arg Asp Glu Ala Thr 690 695 700		

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Tyr Lys Val Pro Leu Asp Thr Thr Glu Tyr Pro Glu Glu Gln Tyr Val
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 5 Ser Asp Ile Leu Asn Tyr Ile Asp His Gly Asp Pro Gln Val Arg Gly
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 Ala Thr Ala Ile Leu Cys Gly Thr Leu Ile Cys Ser Ile Leu Ser Arg
 770 775 780
 10 Ser Arg Phe His Val Gly Asp Trp Met Gly Thr Ile Arg Thr Leu Thr
 785 790 795 800
 Gly Asn Thr Phe Ser Leu Ala Asp Cys Ile Pro Leu Leu Arg Lys Thr
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 15 Leu Lys Asp Glu Ser Ser Val Thr Cys Lys Leu Ala Cys Thr Ala Val
 820 825 830
 Arg Asn Cys Val Met Ser Leu Cys Ser Ser Ser Tyr Ser Glu Leu Gly
 835 840 845
 20 Leu Gln Leu Ile Ile Asp Val Leu Thr Leu Arg Asn Ser Ser Tyr Trp
 850 855 860
 Leu Val Arg Thr Glu Leu Leu Glu Thr Leu Ala Glu Ile Asp Phe Arg
 865 870 875 880
 25 Leu Val Ser Phe Leu Glu Ala Lys Ala Glu Asn Leu His Arg Gly Ala
 885 890 895
 His His Tyr Thr Gly Leu Leu Lys Leu Gln Glu Arg Val Leu Asn Asn
 900 905 910
 30 Val Val Ile His Leu Leu Gly Asp Glu Asp Pro Arg Val Arg His Val
 915 920 925
 Ala Ala Ala Ser Leu Ile Arg Leu Val Pro Lys Leu Phe Tyr Lys Cys
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 Asp Gln Gly Gln Ala Asp Pro Val Val Ala Val Ala Arg Asp Gln Ser
 945 950 955 960
 35 Ser Val Tyr Leu Lys Leu Leu Met His Glu Thr Gln Pro Pro Ser His
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 Phe Ser Val Ser Thr Ile Thr Arg Ile Tyr Arg Gly Tyr Asn Leu Leu
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 40 Pro Ser Ile Thr Asp Val Thr Met Glu Asn Asn Leu Ser Arg Val Ile
 995 1000 1005
 Ala Ala Val Ser His Glu Leu Ile Thr Ser Thr Thr Arg Ala Leu Thr
 1010 1015 1020
 45 Phe Gly Cys Cys Glu Ala Leu Cys Leu Leu Ser Thr Ala Phe Pro Val
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 Lys Ile Trp Ser Leu Gly Trp His Cys Gly Val Pro Pro Leu Ser Ala

His Asp Ala Leu Ile Leu Ala Gly Asn Leu Leu Ala Ala Ser Ala Pro

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Ala Thr Lys Gln Glu Glu Val Trp Pro Ala Leu Gly Asp Arg Ala Leu
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Val Pro Met Val Glu Gln Leu Phe Ser His Leu Leu Lys Val Ile Asn
1140 1145 1150

Ile Cys Ala His Val Leu Asp Asp Val Ala Pro Gly Pro Ala Ile Lys
1155 1160 1165

Ala Ala Leu Pro Ser Leu Thr Asn Pro Pro Ser Leu Ser Pro Ile Arg
1170 1175 1180

Arg Lys Gly Lys Glu Lys Glu Pro Gly Glu Gln Ala Ser Val Pro Leu
1185 1190 1195 1200

Ser Pro Lys Lys Gly Ser Glu Ala Ser Ala Ala Ser Arg Gln Ser Asp
1205 1210 1215

Thr Ser Gly Pro Val Thr Thr Ser Lys Ser Ser Ser Leu Gly Ser Phe
1220 1225 1230

Tyr His Leu Pro Ser Tyr Leu Arg Leu His Asp Val Leu Lys Ala Thr
1235 1240 1245

His Ala Asn Tyr Lys Val Thr Leu Asp Leu Gln Asn Ser Thr Glu Lys
1250 1255 1260

Phe Gly Gly Phe Leu Arg Ser Ala Leu Asp Val Leu Ser Gln Ile Leu
1265 1270 1275 1280

Glu Leu Ala Thr Leu Gln Asp Ile Gly Lys Cys Val Glu Glu Ile Leu
1285 1290 1295

Gly Tyr Leu Lys Ser Cys Phe Ser Arg Glu Pro Met Met Ala Thr Val
1300 1305 1310

Cys Val Gln Gln Leu Leu Lys Thr Leu Phe Gly Thr Asn Leu Ala Ser
1315 1320 1325

Gln Phe Asp Gly Leu Ser Ser Asn Pro Ser Lys Ser Gln Gly Arg Ala
1330 1335 1340

Gln Arg Leu Gly Ser Ser Ser Val Arg Pro Gly Leu Tyr His Tyr Cys
1345 1350 1355 1360

Phe Met Ala Pro Tyr Thr His Phe Thr Gln Ala Leu Ala Asp Ala Ser
1365 1370 1375

Leu Arg Asn Met Val Gln Ala Glu Gln Glu Asn Asp Thr Ser Gly Trp
1380 1385 1390

Phe Asp Val Leu Gln Lys Val Ser Thr Gln Leu Lys Thr Asn Leu Thr
1395 1400 1405

Ser Val Thr Lys Asn Arg Ala Asp Lys Asn Ala Ile His Asn His Ile
1410 1415 1420

Arg Leu Phe Glu Pro Leu Val Ile Lys Ala Leu Lys Gln Tyr Thr Thr
1425 1430 1435 1440

Ile Ile Gly Ile Val Leu Tyr Ile Asn Ala Tyr Ile Gln Val Gly Gln
1445 1450 1455

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Leu Leu Ser Tyr Glu Arg Tyr His Ser Lys Gln Ile Ile Gly Ile Pro
1505 1510 1515 1520

Lys Ile Ile Gln Leu Cys Asp Gly Ile Met Ala Ser Gly Arg Lys Ala
1525 1530 1535

Val Thr His Ala Ile Pro Ala Leu Gln Pro Ile Val His Asp Leu Phe
1540 1545 1550

Val Leu Arg Gly Thr Asn Lys Ala Asp Ala Gly Lys Glu Leu Glu Thr
1555 1560 1565

Gln Lys Glu Val Val Val Ser Met Leu Leu Arg Leu Ile Gln Tyr His
1570 1575 1580

Gln Val Leu Glu Met Phe Ile Leu Val Leu Gln Gln Cys His Lys Glu
1585 1590 1595 1600

Asn Glu Asp Lys Trp Lys Arg Leu Ser Arg Gln Ile Ala Asp Ile Ile
1605 1610 1615

Leu Pro Met Leu Ala Lys Gln Gln Met His Ile Asp Ser His Glu Ala
1620 1625 1630

Leu Gly Val Leu Asn Thr Leu Phe Glu Ile Leu Ala Pro Ser Ser Leu
1635 1640 1645

Arg Pro Val Asp Met Leu Leu Arg Ser Met Phe Val Thr Pro Asn Thr
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Met Ala Ser Val Ser Thr Val Gln Leu Trp Ile Ser Gly Ile Leu Ala
1665 1670 1675 1680

Ile Leu Arg Val Leu Ile Ser Gln Ser Thr Glu Asp Ile Val Leu Ser
1685 1690 1695

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1700 1705 1710

Ile Asn Arg Leu Arg Asp Gly Asp Ser Thr Ser Thr Leu Glu Glu His
1715 1720 1725

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1730 1735 1740

Phe Leu Leu Gln Leu Val Gly Ile Leu Leu Glu Asp Ile Val Thr Lys
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Gln Leu Lys Val Glu Met Ser Glu Gln Gln His Thr Phe Tyr Cys Gln
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Glu Leu Gly Thr Leu Leu Met Cys Leu Ile His Ile Phe Lys Ser Gly
1780 1785 1790

Met Phe Arg Arg Ile Thr Ala Ala Ala Thr Arg Leu Phe Arg Ser Asp
1795 1800 1805

Gly Cys Gly Gly Ser Phe Tyr Thr Leu Asp Ser Leu Asn Leu Arg Ala
1810 1815 1820

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Gly Met Cys Asn Arg Glu Ile Val Arg Arg Gly Ala Leu Ile Leu Phe
 1890 1895 1900
 Cys Asp Tyr Val Cys Gln Asn Leu His Asp Ser Glu His Leu Thr Trp
 1905 1910 1915 1920
 5
 Leu Ile Val Asn His Ile Gln Asp Leu Ile Ser Leu Ser His Glu Pro
 1925 1930 1935
 Pro Val Gln Asp Phe Ile Ser Ala Val His Arg Asn Ser Ala Ala Ser
 1940 1945 1950
 10
 Gly Leu Phe Ile Gln Ala Ile Gln Ser Arg Cys Glu Asn Leu Ser Thr
 1955 1960 1965
 Pro Thr Met Leu Lys Lys Thr Leu Gln Cys Leu Glu Gly Ile His Leu
 1970 1975 1980
 15
 Ser Gln Ser Gly Ala Val Leu Thr Leu Tyr Val Asp Arg Leu Leu Cys
 1985 1990 1995 2000
 Thr Pro Phe Arg Val Leu Ala Arg Met Val Asp Ile Leu Ala Cys Arg
 2005 2010 2015
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 Arg Val Glu Met Leu Leu Ala Ala Asn Leu Gln Ser Ser Met Ala Gln
 2020 2025 2030
 Leu Pro Met Glu Glu Leu Asn Arg Ile Gln Glu Tyr Leu Gln Ser Ser
 2035 2040 2045
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 Gly Leu Ala Gln Arg His Gln Arg Leu Tyr Ser Leu Leu Asp Arg Phe
 2050 2055 2060
 Arg Leu Ser Thr Met Gln Asp Ser Leu Ser Pro Ser Pro Pro Val Ser
 2065 2070 2075 2080
 30
 Ser His Pro Leu Asp Gly Asp Gly His Val Ser Leu Glu Thr Val Ser
 2085 2090 2095
 Pro Asp Lys Asp Trp Tyr Val His Leu Val Lys Ser Gln Cys Trp Thr
 2100 2105 2110
 35
 Arg Ser Asp Ser Ala Leu Leu Glu Gly Ala Glu Leu Val Asn Arg Ile
 2115 2120 2125
 Pro Ala Glu Asp Met Asn Ala Phe Met Met Asn Ser Glu Phe Asn Leu
 2130 2135 2140
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 Ser Leu Leu Ala Pro Cys Leu Ser Leu Gly Met Ser Glu Ile Ser Gly
 2145 2150 2155 2160
 Gly Gln Lys Ser Ala Leu Phe Glu Ala Ala Arg Glu Val Thr Leu Ala
 2165 2170 2175
 45
 Arg Val Ser Gly Thr Val Gln Gln Leu Pro Ala Val His His Val Phe
 2180 2185 2190
 Gln Pro Glu Leu Pro Ala Glu Pro Ala Ala Tyr Trp Ser Lys Leu Asn
 2195 2200 2205
 55
 Ser Phe Leu Ile Thr Val Tyr Val Val Val Val Val Val Val Val Val Val
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Leu Ser Leu Asp Leu Gln Ala Gly Leu Asp Cys Cys Cys Leu Ala Leu
 2275 2280 2285
 Gln Leu Pro Gly Leu Trp Ser Val Val Ser Ser Thr Glu Phe Val Thr
 2290 2295 2300
 His Ala Cys Ser Leu Ile Tyr Cys Val His Phe Ile Leu Glu Ala Val
 2305 2310 2315 2320
 Ala Val Gln Pro Gly Glu Gln Leu Leu Ser Pro Glu Arg Arg Thr Asn
 2325 2330 2335
 Thr Pro Lys Ala Ile Ser Glu Glu Glu Glu Glu Val Asp Pro Asn Thr
 2340 2345 2350
 Gln Asn Pro Lys Tyr Ile Thr Ala Ala Cys Glu Met Val Ala Glu Met
 2355 2360 2365
 Val Glu Ser Leu Gln Ser Val Leu Ala Leu Gly His Lys Arg Asn Ser
 2370 2375 2380
 Gly Val Pro Ala Phe Leu Thr Pro Leu Leu Arg Asn Ile Ile Ile Ser
 2385 2390 2395 2400
 Leu Ala Arg Leu Pro Leu Val Asn Ser Tyr Thr Arg Val Pro Pro Leu
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 Val Trp Lys Leu Gly Trp Ser Pro Lys Pro Gly Gly Asp Phe Gly Thr
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 Ala Phe Pro Glu Ile Pro Val Glu Phe Leu Gln Glu Lys Glu Val Phe
 2435 2440 2445
 Lys Glu Phe Ile Tyr Arg Ile Asn Thr Leu Gly Trp Thr Ser Arg Thr
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 Gln Phe Glu Glu Thr Trp Ala Thr Leu Leu Gly Val Leu Val Thr Gln
 2465 2470 2475 2480
 Pro Leu Val Met Glu Gln Glu Glu Ser Pro Pro Glu Glu Asp Thr Glu
 2485 2490 2495
 Arg Thr Gln Ile Asn Val Leu Ala Val Gln Ala Ile Thr Ser Leu Val
 2500 2505 2510
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 Leu Glu Gln Gln Pro Arg Asn Lys Pro Leu Lys Ala Leu Asp Thr Arg
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 Phe Gly Arg Lys Leu Ser Ile Ile Arg Gly Ile Val Glu Gln Glu Ile
 2545 2550 2555 2560
 Gln Ala Met Val Ser Lys Arg Glu Asn Ile Ala Thr His His Leu Tyr
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 Gln Ala Trp Asp Pro Val Pro Ser Leu Ser Pro Ala Thr Thr Gly Ala
 2580 2585 2590
 Trp Leu Val Asn Ser Ile Thr Ser Val Arg Ser Glu Glu Trp Asp Ile
 2625 2630 2635 2640

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Ser Pro Val Asn Ser Arg Lys His Arg Ala Gly Val Asp Ile His Ser
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 Cys Ser Gln Phe Leu Leu Glu Leu Tyr Ser Arg Trp Ile Leu Pro Ser
 2675 2680 2685
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 Asp Glu Ile Leu Ala Gln Tyr Leu Val Pro Ala Thr Cys Lys Ala Ala
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 Lys Gly Ile Ala His Cys Val Asn Ile His Ser Gln Gln His Val Leu
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 Val Met Cys Ala Thr Ala Phe Tyr Leu Ile Glu Asn Tyr Pro Leu Asp
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 Val Gly Pro Glu Phe Ser Ala Ser Ile Ile Gln Met Cys Gly Val Met
 2850 2855 2860
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 55
 Tyr Thr Glu Ile Met Ala Thr Val Val Tyr Lys Val Ile Thr Thr
 2980 2985 2990

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Ser Leu Ser Asn Phe Thr Gln Arg Ala Pro Val Ala Met Ala Thr Trp
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 Ser Leu Ser Cys Phe Phe Val Ser Ala Ser Thr Ser Pro Trp Val Ala
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 Asp Val Asn Leu Phe Cys Leu Val Ala Thr Asp Phe Tyr Arg His Gln
 3090 3095 3100
 10
 Ile Glu Glu Glu Leu Asp Arg Arg Ala Phe Gln Ser Val Leu Glu Val
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 Val Ala Ala Pro Gly Ser Pro Tyr His Arg Leu Leu Thr Cys Leu Arg
 3125 3130 3135
 15
 Asn Val His Lys Val Thr Thr Cys
 3140

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Claims

- 5 1. An isolated, purified or recombinant polypeptide comprising a huntingtin protein or a mutant, fragment or variant thereof having substantially the same activity as huntingtin protein.
2. A polypeptide according to claim 1 having the amino acid sequence shown in SEQ ID NO:6.
- 10 3. A polypeptide according to claim 1 or 2 which is essentially purified and/or has at least 5 contiguous amino acids.
4. An isolated, purified or recombinant nucleic acid molecule comprising nucleic acid which is:
 - 15 (a) a sequence encoding a huntingtin protein according to any preceding claim (whether normal or genetically defective), or its complementary strand;
 - (b) a sequence that is substantially homologous to, or hybridises under stringent conditions to, either sequence in (a);
 - (c) a sequence that is substantially homologous to, or would hybridise under stringent conditions to, a sequence in (a) or (b) but for the degeneracy of the genetic code;
 - 20 or a fragment of any of (a), (b) or (c).
5. A nucleic acid according to claim 1, wherein the huntingtin protein has the amino acid sequence shown in SEQ ID NO:6 and/or the nucleic acid is DNA encoding the amino acid sequence SEQ ID NO:5.
- 25 6. A nucleic acid molecule according to claim 4 or 5 which is a probe for detecting the presence of huntingtin in a sample comprising being at least 5, such as at least 15, contiguous nucleotides.
7. A (preferably recombinant) nucleic acid molecule according to any of claims 4 to 6 comprising a transcriptional region functional in a cell operably linked to a sequence complementary to an RNA sequence encoding a protein according to any of claims 1 to 3 or at least 5 contiguous amino acids thereof.
- 30 8. A vector comprising a nucleic acid molecule according to any of claims 4 to 7.
9. A vector according to claim 8 wherein the nucleic acid molecule, such as encoding huntingtin protein, is operably linked to transcriptional and/or translational expression signals.
- 35 10. A host cell transformed or transfected with a vector according to claim 4 or 5.
11. An antibody specific for huntingtin protein, or a protein according to any of claims 1 to 3.
- 40 12. A hybridoma which produces an antibody according to claim 11.
13. A method of detecting the presence of, or predisposition to develop, Huntington's disease in a subject, the method comprising evaluating the characteristics of huntingtin nucleic acid in a sample from the subject, for example in relation to the number of (CAG) repeats.
- 45 14. A method according to claim 13 comprising:
 - (a) taking a sample from the subject;
 - (b) evaluating the characteristics of huntingtin nucleic acid in the sample, wherein the evaluation comprises detecting the huntingtin (CAG) region in the sample; and
15. A method according to claim 13 comprising:
 - 55 (a) taking a sample from a subject and;
 - (b) evaluating the characteristics of huntingtin nucleic acid in the sample, wherein the evaluation comprises detecting the huntingtin (CAG) region in the sample; and

16. The use of:
 - (a) a nucleic acid molecule according to any of claims 4 to 6 or a vector according to claim 8 which encodes a functional (or non-defective) protein;
 - (b) a polypeptide according to any of claims 1 to 3 which is functional (or non-defective);
 - 5 (c) a host cell according to claim 10 expressing a polypeptide which is functional (or non-defective); and/or
 - (d) an antagonist to, or a compound that binds to, huntingdon protein;in the preparation of an agent for treating, delaying or preventing a neurodegenerative disorder.
- 10 17. The use according to claim 16 which is gene therapy.
18. The use according to claim 16 or 17 for treating, preventing or delaying Huntingdon's disease.
19. The use according to any of claims 16 to 17 wherein the nucleic acid has from 11 to 34 (CAG) repeats
15 and/or the polypeptide has from 11 to 34 Gln repeats, said repeats being consecutive.
20. A diagnostic and/or immunoassay kit comprising at least one container and;
 - (a) a nucleic acid molecule according to any of claims 4 to 6, optionally labelled; or
 - (b) an antibody according to claim 11, optionally labelled.
- 20 21. The use of:
 - (a) a nucleic acid molecule according to any of claims 4 to 6 or a vector according to claim 8 which encodes a functional (or non-defective) protein;
 - (b) a polypeptide according to any of claims 1 to 3 which is functional (or non-defective);
 - 25 (c) a host cell according to claim 10 expressing a polypeptide which is functional (or non-defective); and/or
 - (d) an antagonist to, or a compound that binds to, huntingdon protein;in the preparation of a medicament.
22. A pharmaceutical composition comprising:
 - 30 (a) a nucleic acid molecule according to any of claims 4 to 6 or a vector according to claim 8 which encodes a functional (or non-defective) protein;
 - (b) a polypeptide according to any of claims 1 to 3 which is functional (or non-defective);
 - (c) a host cell according to claim 10 expressing a polypeptide which is functional (or non-defective);
 - 35 (d) an antagonist to, or a compound that binds to, huntingdon protein;in admixture with pharmaceutically acceptable carrier.
23. A process for the preparation of a polypeptide, the process comprising culturing a host cell according to claim 10 under conditions whereby the polypeptide is expressed, and purifying or isolating the polypep-
40 tide.

45

55

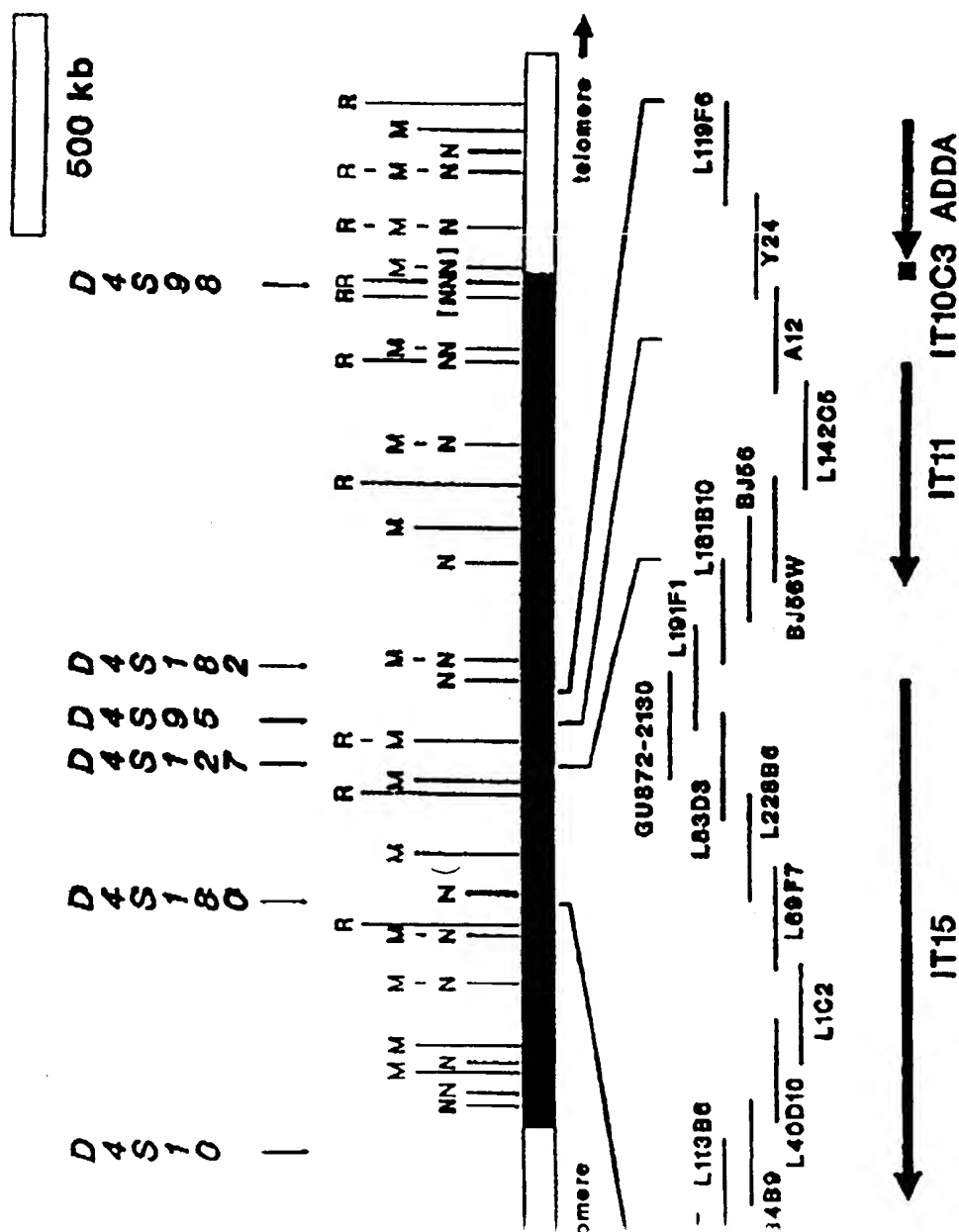


FIGURE 1

1 2 3



— 28S



— 18S

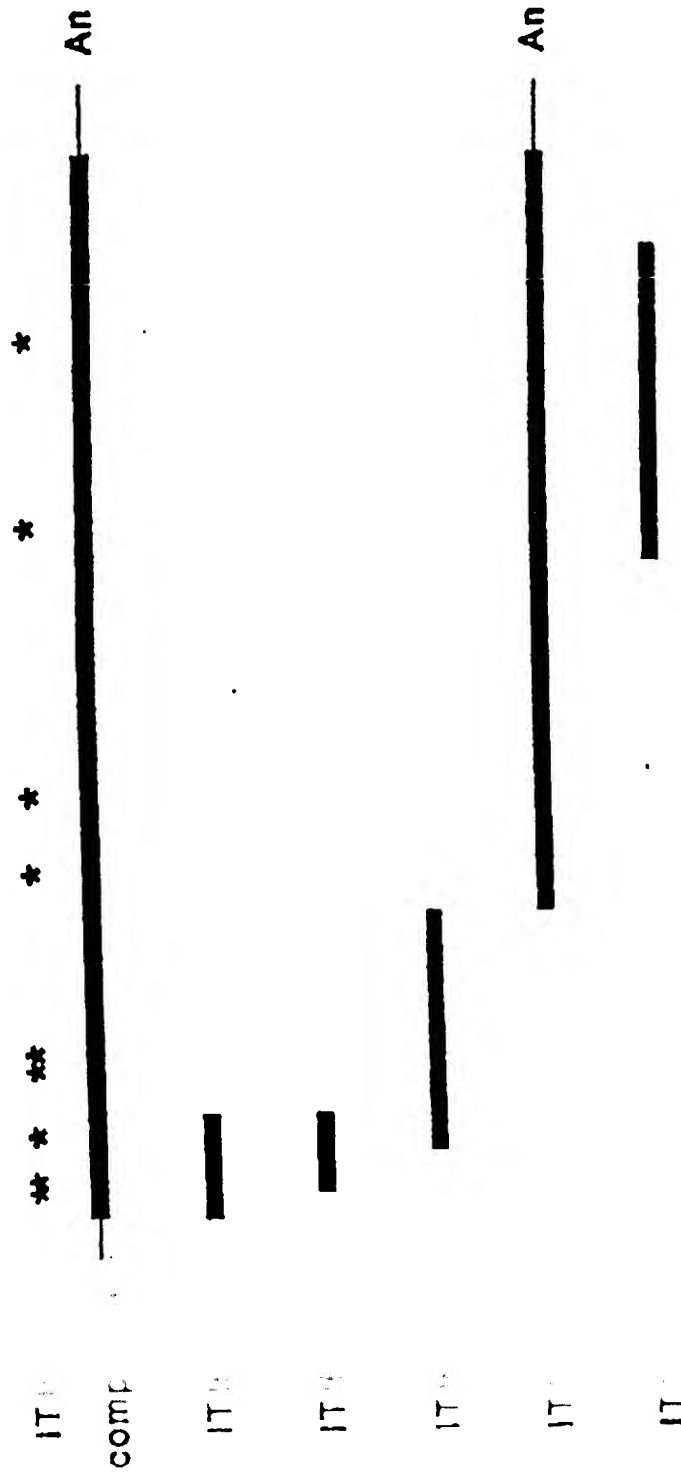


Figure 3.

[illegible]

FIGURE 4 (Sheet 1 of 3)

[illegible]

FIGURE 4 (Sheet 2 of 3)

50



FIGURE 6

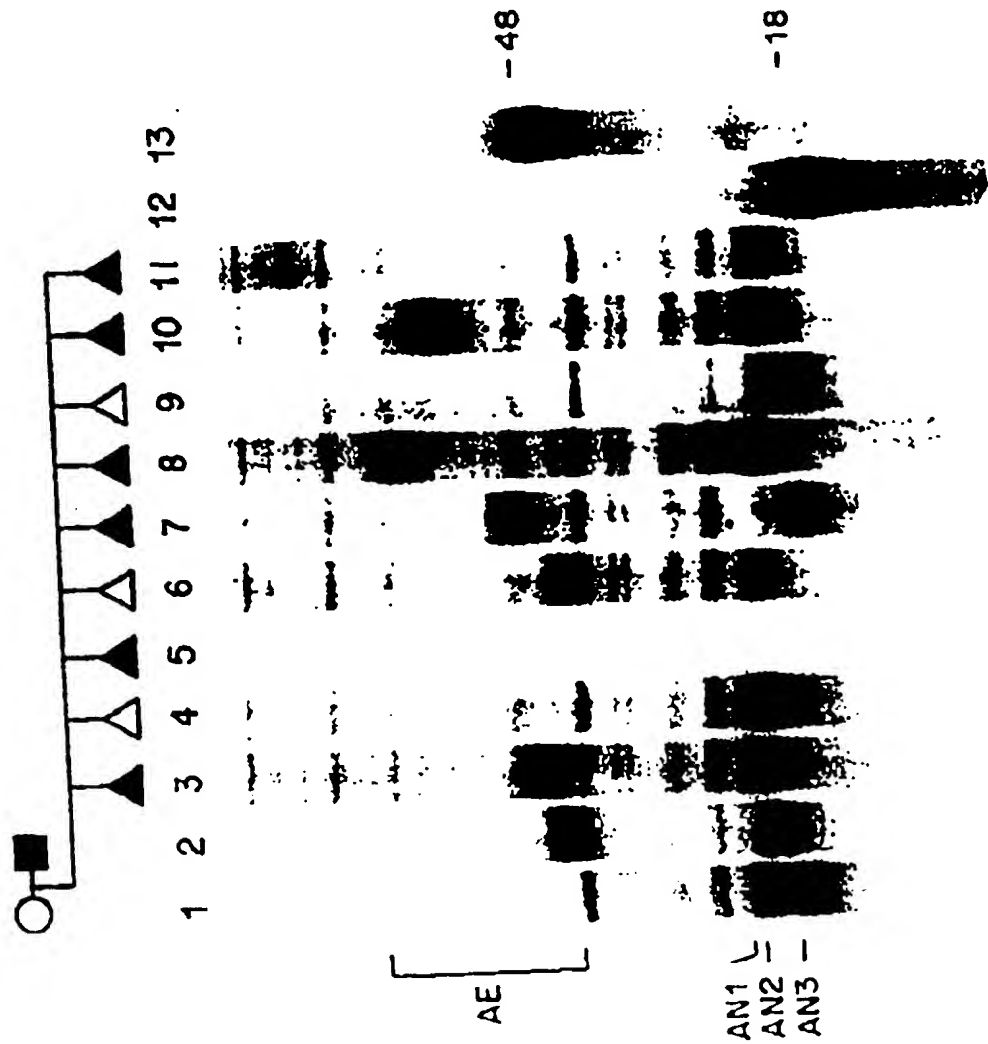


FIGURE 7

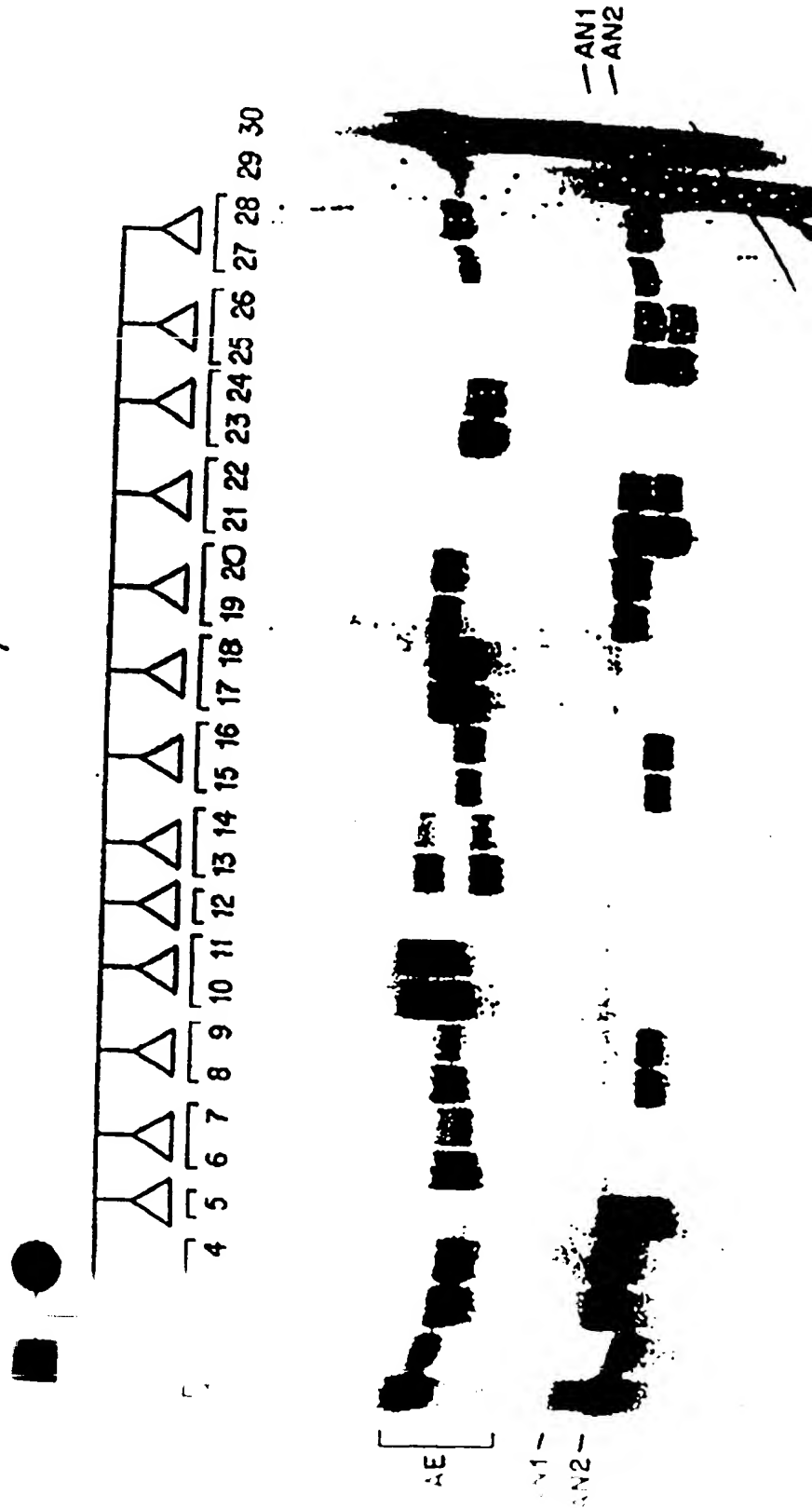




FIGURE 9

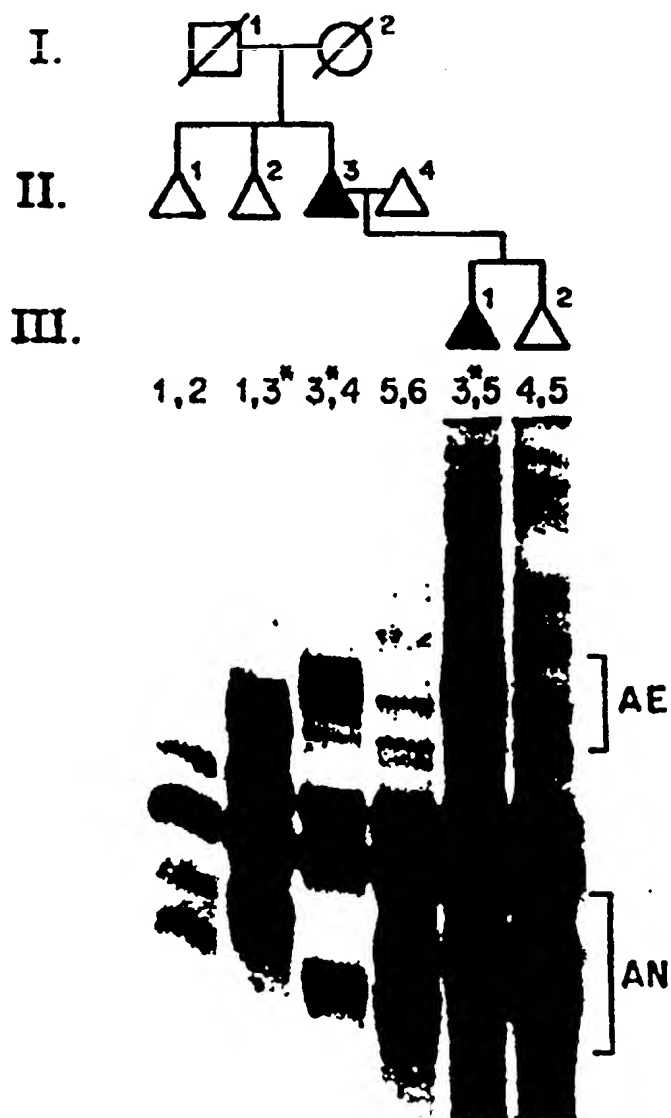


FIGURE 10



FIGURE 11

■ Control chromosomes □ HD chromosomes

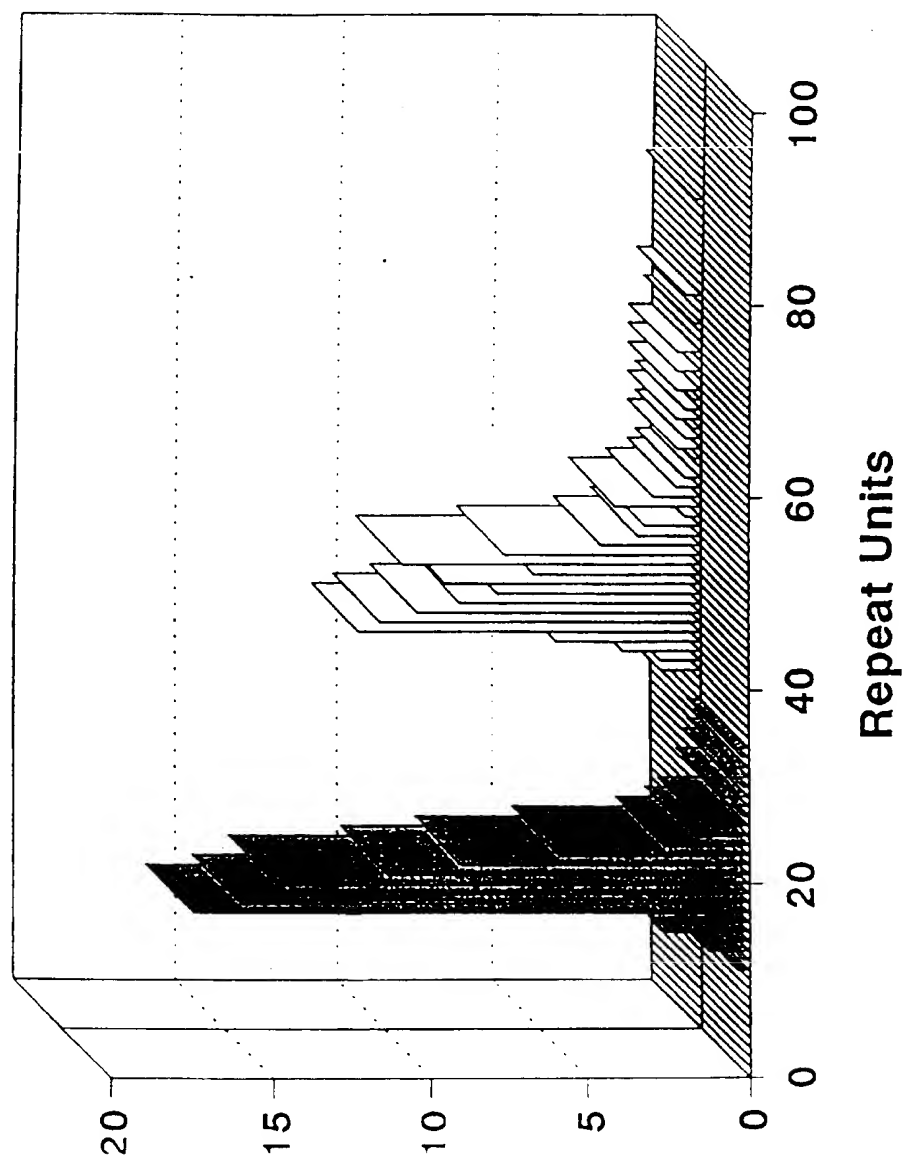


FIGURE 12 (PANEL A)

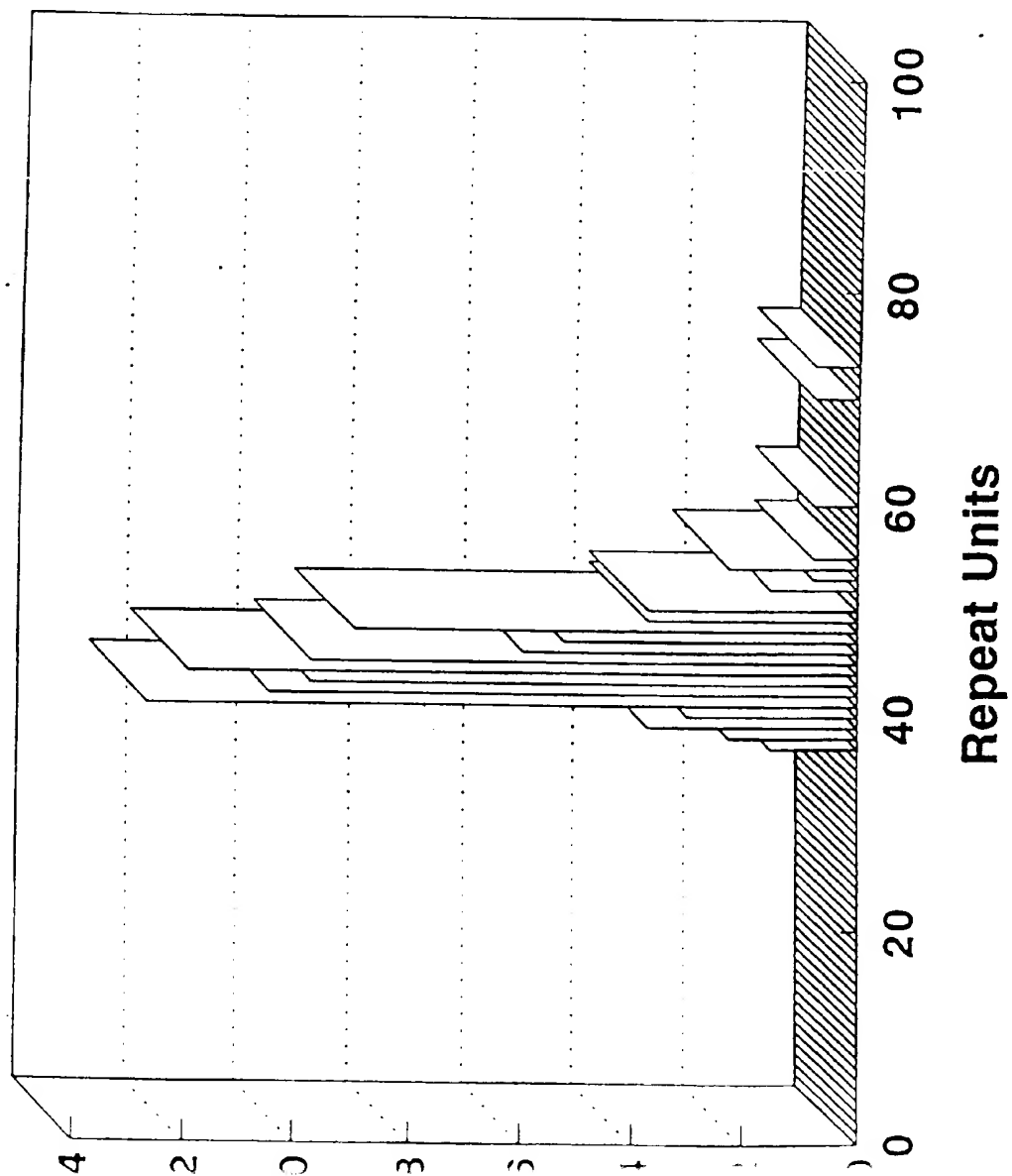


FIGURE 12 cont. (PANEL B)

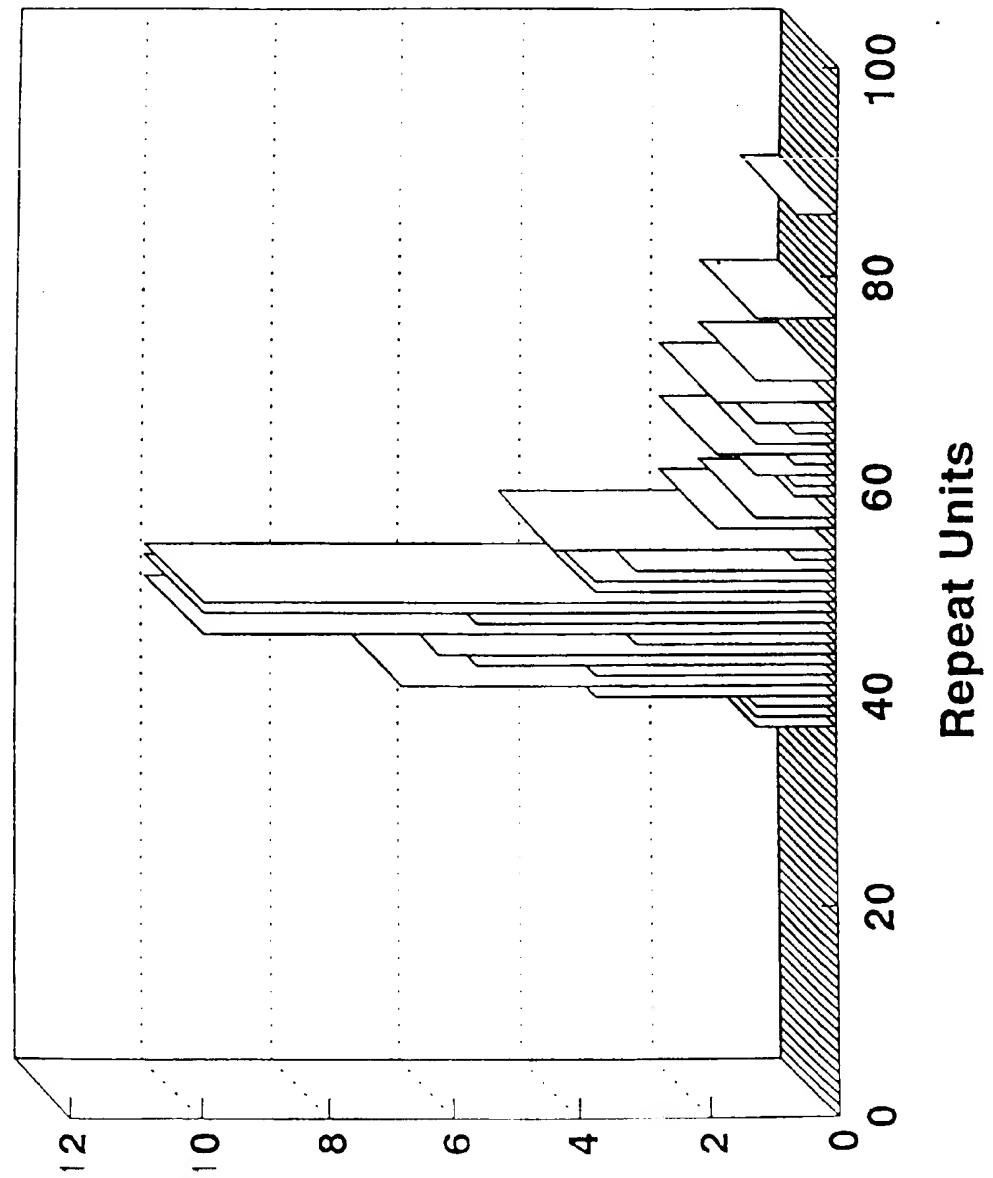


FIGURE 13 (PANEL A)

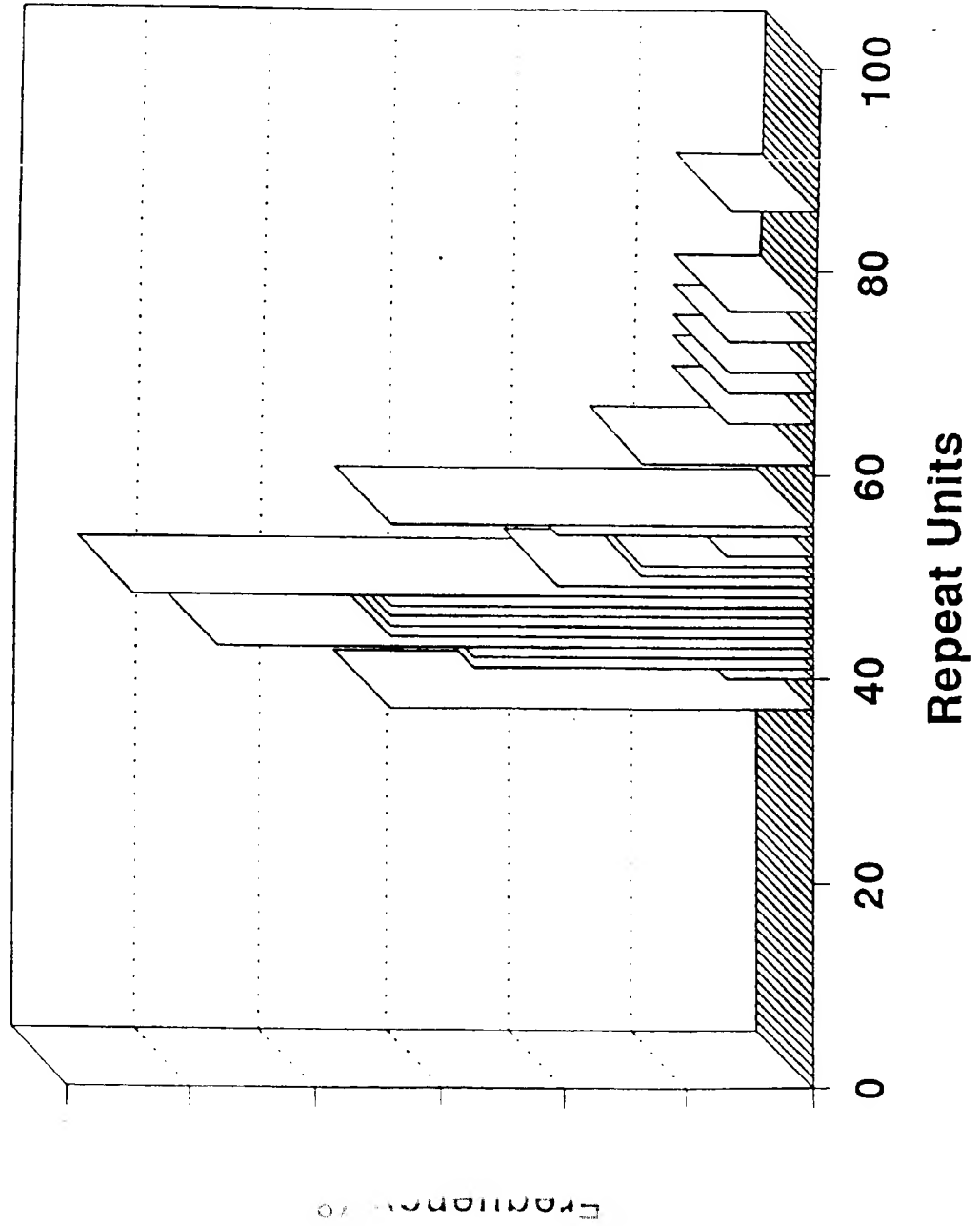


FIGURE 13 cont. (PANEL B)

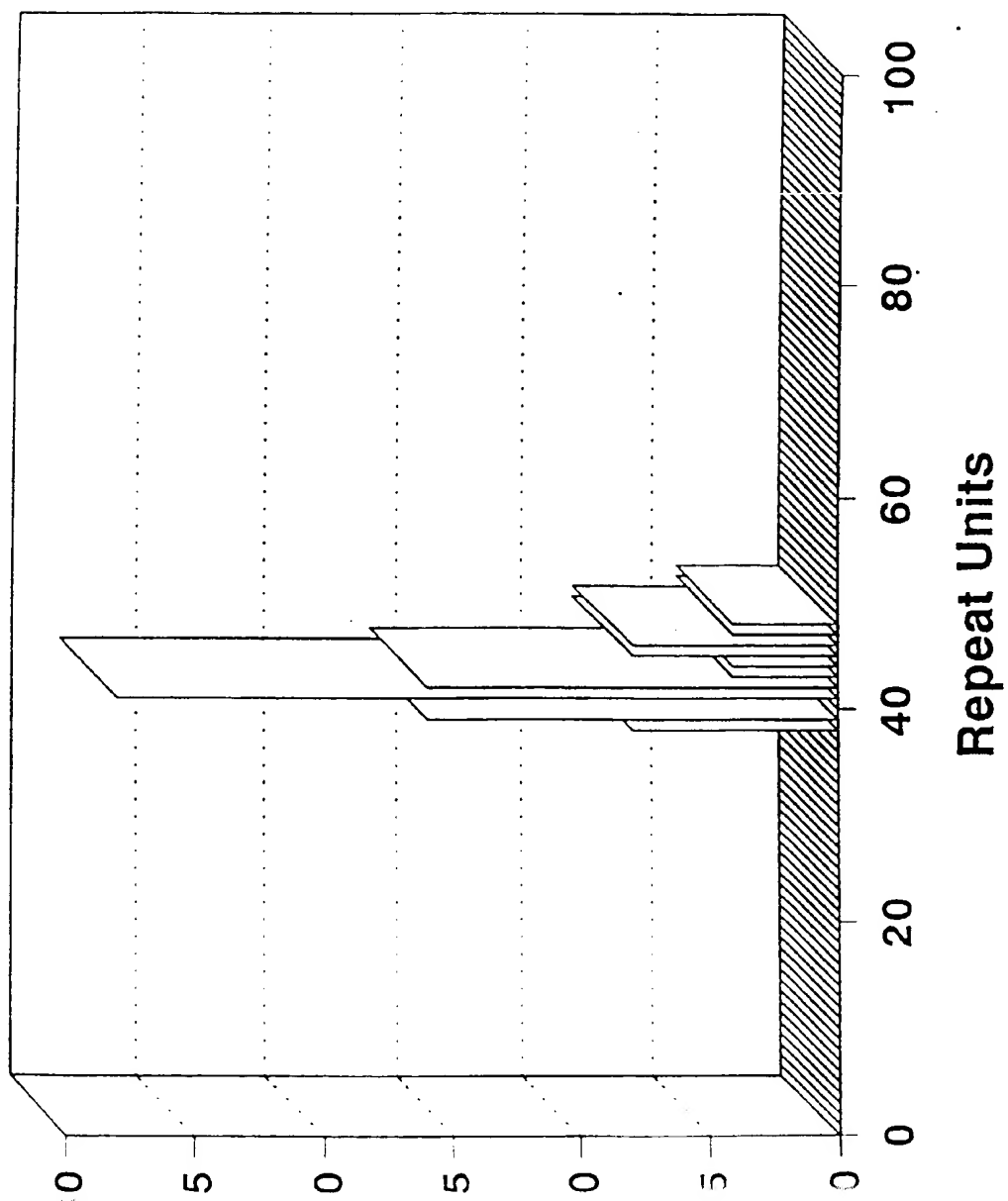


FIGURE 13 cont. (PANEL C)

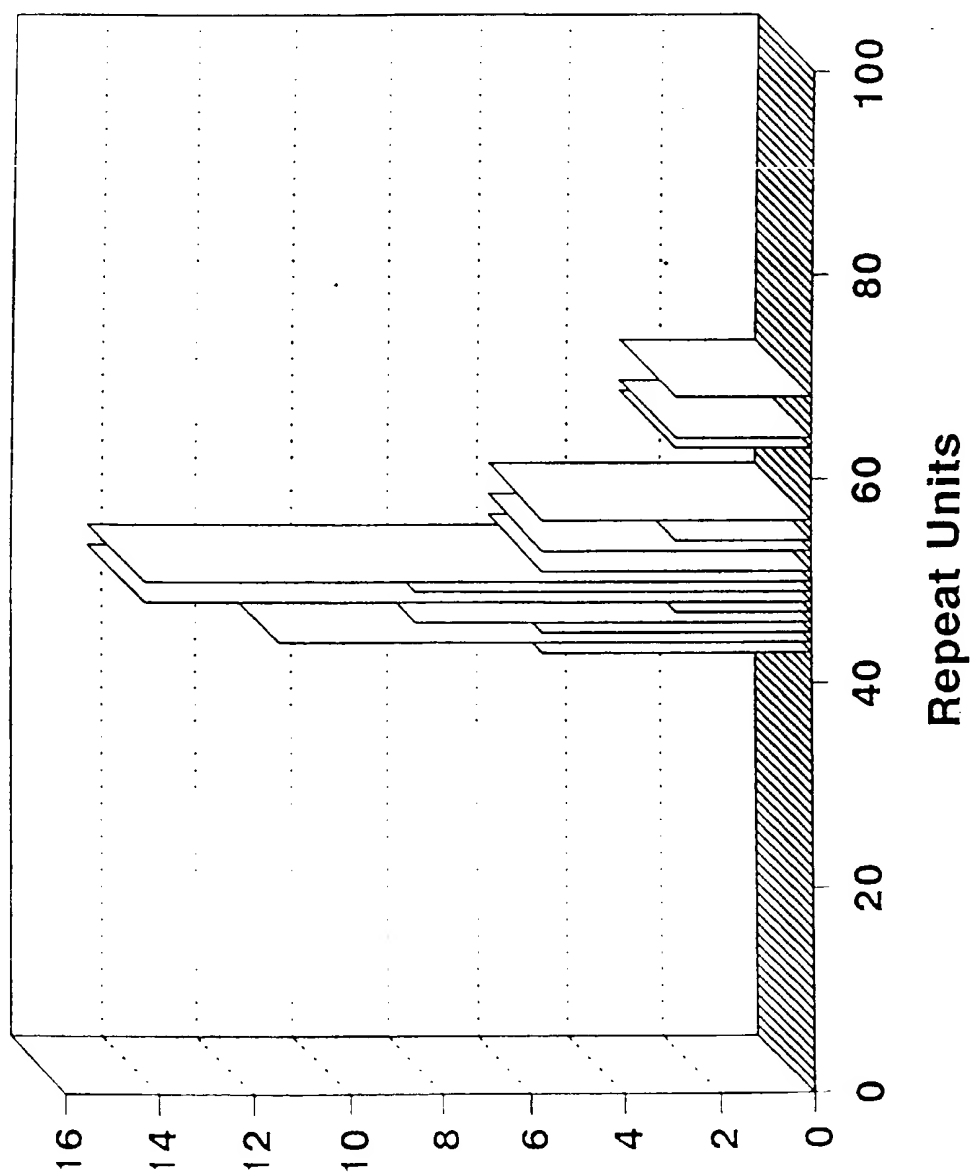


FIGURE 14 (PANEL A)

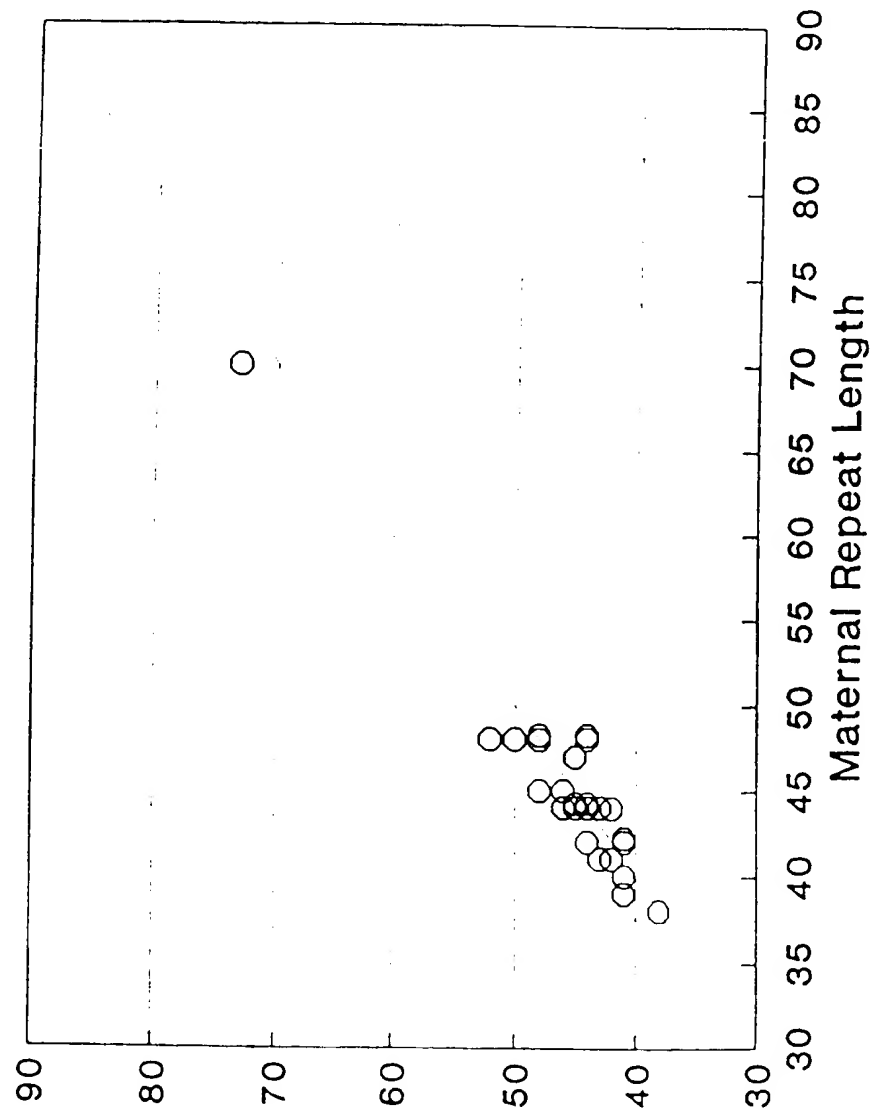


FIGURE 14 cont. (PANEL B)

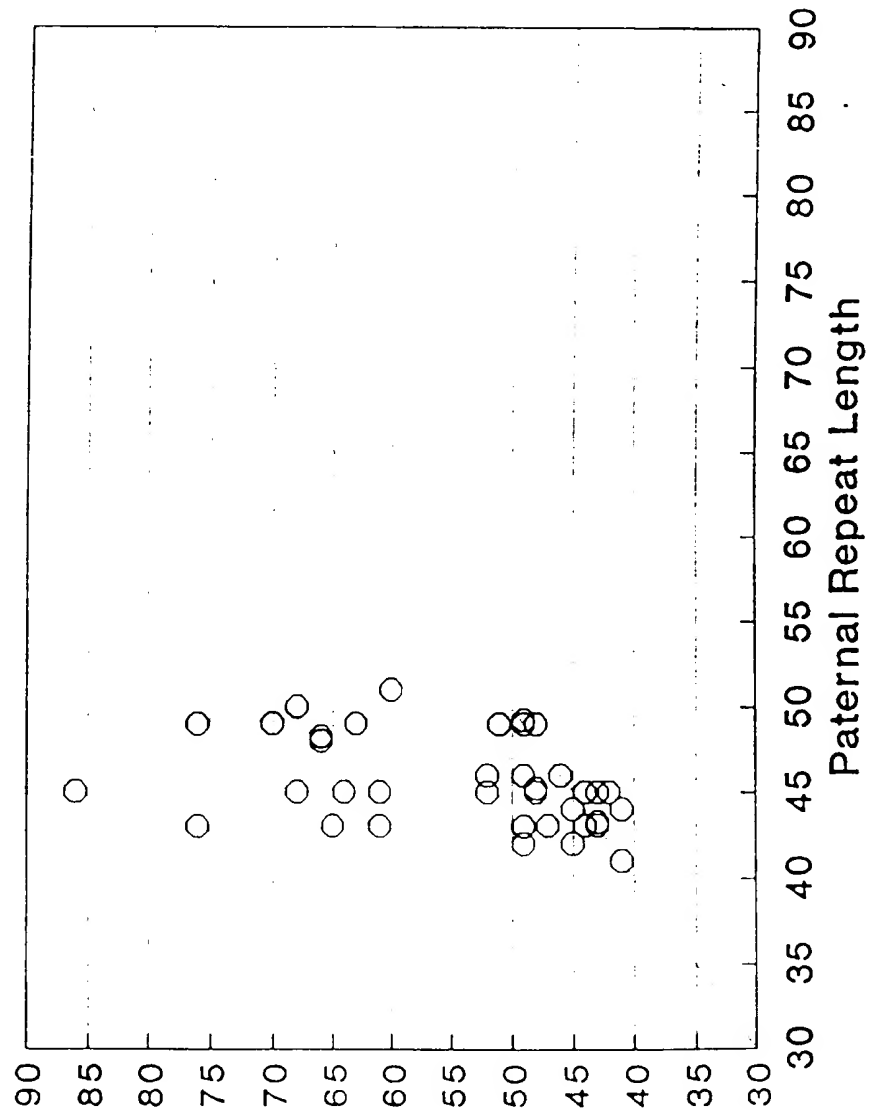


FIGURE 15

1	2	3	4	5	
┌───┐		┌───┐		┌───┐	
S	L	S	L	S	L

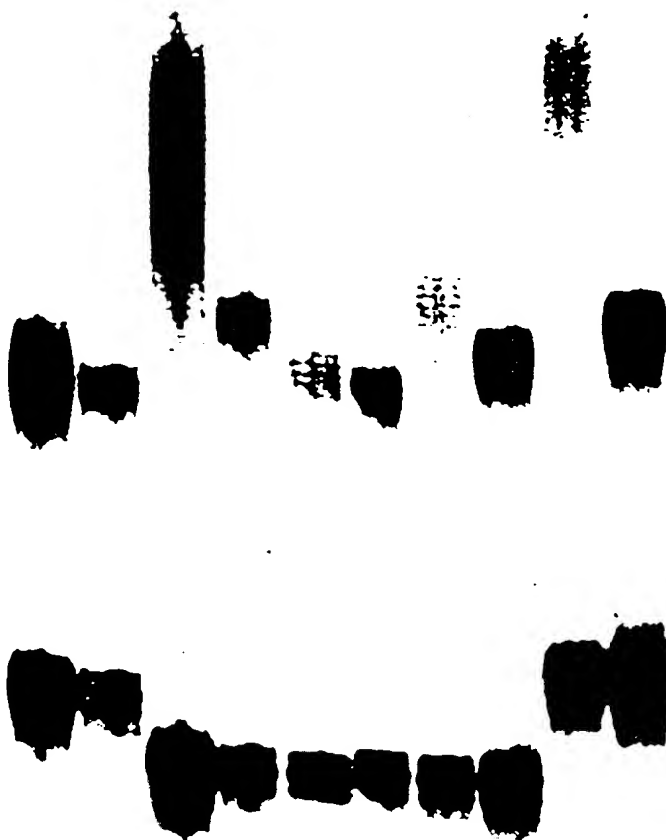


FIGURE 16

